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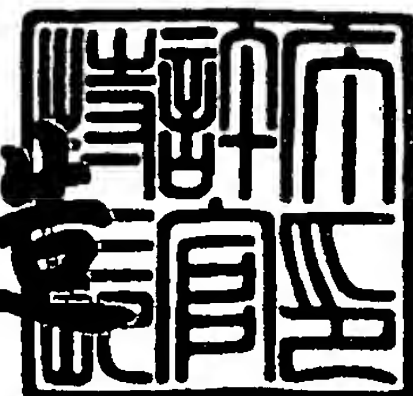
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【発明の名称】 新規遺伝子

【特許請求の範囲】

【請求項 1】 以下の (a) または (b) の精製されかつ単離されたタンパク質。

(a) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 で表されるアミノ酸配列からなるタンパク質。

(b) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 において 1 若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつ NF- $\kappa$ B (Nuclear factor kappa B) を活性化作用を有するタンパク質。

【請求項 2】 請求項 1 記載のタンパク質とその全長にわたり 95% 以上のアミノ酸配列の同一性を有するタンパク質であり、かつ NF- $\kappa$ B を活性化作用を有する

作用を有する精製されかつ単離されたタンパク質。

【請求項3】 以下の（a）または（b）のタンパク質をコードするヌクレオチド配列を包含する単離されたポリヌクレオチド。

（a）配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質。

（b）配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178において1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質。

【請求項4】 以下の（a）～（c）のいずれかのポリヌクレオチド配列を含む単離されたポリヌクレオチド。

（a）配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、

72、74、76、78、80、82、84、86、88、90、92、94、  
 96、98、100、102、104、106、108、110、112、11  
 4、116、118、120、122、124、126、128、130、13  
 2、134、136、138、140、142、144、146、148、15  
 0、151、153、155、157、159、161、163、165、16  
 7、169、171、173、175または177で表されるポリヌクレオチド  
 配列および該ポリヌクレオチド配列に相補的なポリヌクレオチド配列。

(b) (a) のポリヌクレオチド配列を有するポリヌクレオチドとストリンジェ  
 ントな条件下でハイブリダイズし、かつNF- $\kappa$ Bを活性化する作用を有するタ  
 ンパク質をコードするポリヌクレオチド配列。

(c) 配列番号2、4、6、8、10、12、14、16、18、20、22、  
 24、26、28、30、32、34、36、38、40、42、44、46、  
 48、50、52、54、56、58、60、62、64、66、68、70、  
 72、74、76、78、80、82、84、86、88、90、92、94、  
 96、98、100、102、104、106、108、110、112、11  
 4、116、118、120、122、124、126、128、130、13  
 2、134、136、138、140、142、144、146、148、15  
 0、151、153、155、157、159、161、163、165、16  
 7、169、171、173、175または177において、1若しくは複数個  
 のヌクレオチドが欠失、置換若しくは付加されたポリヌクレオチド配列からなり  
 、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするポリヌクレ  
 オチド配列。

【請求項5】 請求項3記載のポリヌクレオチドと全長にわたり少なくとも  
 95%以上の同一性を有し、かつNF- $\kappa$ Bを活性化する作用を有するタンパク  
 質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

【請求項6】 請求項4記載のポリヌクレオチドと全長にわたり少なくとも  
 95%以上の同一性を有し、かつNF- $\kappa$ Bを活性化する作用を有するタンパク  
 質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

【請求項7】 請求項3～6のいずれか1項に記載のポリヌクレオチドによ

リコードされる精製されかつ単離されたタンパク質。

【請求項 8】 請求項 3 ～ 6 のいずれか 1 項に記載のポリヌクレオチドを含有する組換えベクター。

【請求項 9】 請求項 8 に記載の組換えベクターを含む形質転換された細胞

。

【請求項 1 0】 請求項 1 または 2 に記載のタンパク質が膜タンパク質である場合における、請求項 9 記載の細胞の膜。

【請求項 1 1】 (a) 請求項 3 ～ 6 のいずれか 1 項に記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

(b) 培地からタンパク質を回収する、  
ことを含むタンパク質の製造方法。

【請求項 1 2】 (a) 個体のゲノムにおける請求項 1、2 または 7 に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

(b) 該個体に由来するサンプル中での該タンパク質の発現量を分析する、  
ことを含む、該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、発現するタンパク質の量が正常の 2 倍以上あるいは 1 / 2 以下の場合に病気であると診断する方法。

【請求項 1 3】 以下の工程を含む NF- $\kappa$ B 活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

(a) NF- $\kappa$ B を活性化するタンパク質をコードする遺伝子、および NF- $\kappa$ B の活性化に対応した、検出可能シグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

(c) 該形質転換された細胞と 1 あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、および

(e) 該検出可能なシグナルを正常より 2 倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを 2 分の 1 以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程。

【請求項 1 4】 以下の工程を含む、医薬組成物を製造する方法。

(a) NF- $\kappa$ B を活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

(c) 該形質転換された宿主細胞と 1 あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルを正常より 2 倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを 2 分の 1 以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程、  
および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

【請求項 1 5】 NF- $\kappa$ B 活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

(a) NF- $\kappa$ B を活性化するタンパク質をコードする遺伝子、および NF- $\kappa$ B の活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

(b) 検出可能なシグナルを測定するための試薬を含むキット。

【請求項 1 6】 請求項 1、2 または 7 に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

【請求項 1 7】 請求項 1、2 または 7 に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、請求項 1、2 または 7 に記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

【請求項 1 8】 NF- $\kappa$ B の活性化タンパク質の発現を阻害する、請求項 3～6 のいずれか 1 項に記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

【請求項 1 9】 請求項 1、2 または 7 記載のタンパク質をコードする RNA の開裂、または I $\kappa$ B (Inhibitory protein of NF- $\kappa$ B) の分解へ導く経路のタンパク質をコードする RNA の開裂により、NF- $\kappa$ B の活性化を阻害するリボザイム。

【請求項 2 0】 炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される疾患の治療に有効な量の請求項 1 3 記載の方法でスクリーニングされた化合物および／または請求項 1 6 記載のモノクローナルまたはポリクローナル抗体および／または請求項 1 8 記載のアンチセンスオリゴヌクレオチドおよび／または請求項 1 9 記載のリボザイムを個体に投与することを含む疾患の治療法。

【請求項 2 1】 NF- $\kappa$ B の活性化を阻害または活性化するものとして請求項 1 4 に記載の方法により製造された医薬組成物。

【請求項 2 2】 炎症、自己免疫疾患、癌またはウイルス性感染の治療のための請求項 2 1 記載の医薬組成物。

【請求項 2 3】 NF- $\kappa$ B 活性化に関連する疾患を患っている患者に請求項 1 4 記載の方法により製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌およびウイルス性感染を治療する方法。

【請求項 2 4】 GVHD、皮膚疾患、IgA 腎炎、紫斑病性腎炎、増殖性腎炎または劇症肝炎の治療のための請求項 2 1 記載の医薬組成物。

【請求項 2 5】 NF- $\kappa$ B の阻害に関連する疾患を患っている患者に請求項 1 4 記載の方法により製造された化合物を投与することからなる GVHD、皮膚疾患、IgA 腎炎、紫斑病性腎炎、増殖性腎炎または劇症肝炎を治療する方法。

【請求項 2 6】 請求項 1 6 記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

【請求項 2 7】 請求項 1 8 記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。



【請求項 28】 対象疾患が炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される、請求項 26 または 27 に記載の医薬組成物。

【請求項 29】 機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

- (a) オリゴキャッピング法を用いて完全長 cDNA ライブラリーを作製し、
  - (b) 完全長 cDNA および該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに
  - (c) シグナルを発するプラスミドを選択する、
- 方法。

【請求項 30】 配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175 または 177 で表されるヌクレオチド配列のうち少なくとも 1 以上を含むデータセットおよび／または配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 および 178 で表されるアミノ酸配列のうち少なくとも 1 以上を含むデータセットを保存したコンピュータ読み込み可能媒体。



【請求項 3 1】 請求項 3 0 に記載の媒体上のデータと他のヌクレオチド配列および／または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／またはアミノ酸配列との同一性の算出を行う方法。

【請求項 3 2】 配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175 または 177 から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質。

【請求項 3 3】 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

【発明の詳細な説明】

【0001】

【発明の属する技術分野】

本発明は、NF- $\kappa$ B を活性化する作用を有するタンパク質、該タンパク質を

コードするDNA、該DNAの取得方法、該DNAを含有する組換えベクター、該組換えベクターを含有する形質転換体ならびに該タンパク質と特異的に反応する抗体に関する。また、本発明は、NF- $\kappa$ Bの過剰な活性化または阻害が関与する疾患の診断、治療または予防を行う際の本発明のタンパク質、DNAまたは抗体の使用に関する。

## 【0002】

また本発明は、該タンパク質、DNA、組換えベクターおよび形質転換体を用いて、NF- $\kappa$ Bの活性化を阻害または促進する物質をスクリーニングする方法に関する。

## 【0003】

## 【従来の技術】

転写因子NF- $\kappa$ B (Nuclear factor kappa B) は、炎症や免疫反応に関与する種々の遺伝子の転写調節において重要な役割を果たしている。NF- $\kappa$ Bは、Relファミリーに属するホモあるいはヘテロ二量体からなり、無刺激の状態では、制御タンパク質であるI $\kappa$ B (Inhibitory protein of NF- $\kappa$ B) と複合体を形成することによりその核移行シグナルが覆い隠され、細胞質内で不活性型として存在する。

## 【0004】

細胞にインターロイキン (IL) - 1、腫瘍壊死因子 (TNF) -  $\alpha$  などのサイトカインの刺激が与えられると、I $\kappa$ BはIKK (I $\kappa$ B kinase) によってリン酸化され、ユビキチン化を経て26Sプロテアソームにより分解される。これにより遊離されたNF- $\kappa$ Bは核内に移行し、NF- $\kappa$ B結合配列と呼ばれているDNA配列に結合し、その制御下の遺伝子の転写を誘導する。NF- $\kappa$ Bによって発現調節を受けているとされている遺伝子は免疫グロブリン遺伝子の他、IL-1、TNF- $\alpha$  などの炎症性サイトカイン、インターフェロン、細胞接着因子等が知られており、NF- $\kappa$ Bはこれらの遺伝子の発現誘導を介して、炎症や免疫応答に関わっている。

## 【0005】

NF- $\kappa$ Bの機能あるいは活性化を阻害することによって、炎症・免疫疾患や

その他の疾病、たとえば腫瘍増殖、に関与している多くの因子（タンパク質）の発現を抑制できる可能性があり、自己免疫や炎症を原因・症状とする疾病に対する医薬の有望な標的である〔たとえば、*Clinical Chemistry* 45, 7-17 (1999)、*J. Clin. Pharmacol.* 38, 981-993 (1998)、*Gut* 43, 856-860 (1998)、*The New England Journal of Medicine* 366, 1066-1071 (1997)、*TIPS* 46-50 (1997)、*The FASEB Journal* 9, 899-909 (1995)、*Nature* 395, 225-226 (1998)、*Science* 278, 818-819 (1997)、*Cell* 91, 299-302 (1997)〕。

## 【0006】

細胞外からの情報は、何らかのシグナルの形に変えて、細胞膜を通過し細胞質をこえて核に到達し、標的遺伝子の発現を調節して細胞の応答が引き起こされる。そのため、細胞外の刺激からNF- $\kappa$ Bの活性化に至る細胞内におけるシグナル伝達の仕組みを解明することは、自己免疫疾患や炎症症状を呈する疾患に対する新たな医薬の開発あるいは治療法の開発に非常に重要な手段を提供することとなり、極めて重要な意義を有している。

## 【0007】

しかしながら、細胞が一定の刺激を受けてからNF- $\kappa$ Bの活性化に至るまでのシグナル伝達経路にはプロテインキナーゼなどの各種伝達分子が関わる多くのステップの存在が考えられ、従って、より効率的な創薬研究のためには、主要な役割を果たす伝達分子を明らかにした上でそれらに焦点をしばった新しい薬物スクリーニング方法を確立することが望まれる。しかし、NF- $\kappa$ Bの活性化のメカニズムは上記IKK、ユビキチン化酵素、26Sプロテアソームの他、TNF receptor associated factor 2 (TRAF2) やNF- $\kappa$ B inducing kinase (NIK) などの幾つかのシグナル伝達分子が同定され、少しずつ解明されつつあるものの、いまだ不明な点が多く、新たなシグナル伝達分子の同定とより進んだNF- $\kappa$ B活性化メカニズムの解明が望まれていた。

## 【 0 0 0 8 】

## 【発明が解決しようとする課題】

本発明の課題は、上記のように有用なNF- $\kappa$ Bを活性化する作用を有する新規な遺伝子、タンパク質を見出し、これを医薬、診断薬、医療の分野で利用する方法を提供することにある。即ち、NF- $\kappa$ Bを活性化する作用を有する新規タンパク質、該タンパク質をコードするDNA、該DNAを含有する組換えベクター、該組換えベクターを含有する形質転換体、該タンパク質の製造方法、該タンパク質またはその部分ペプチドに対する抗体、該抗体の製造方法を提供する。

## 【 0 0 0 9 】

また、本発明は、該タンパク質、DNA、組換えベクターおよび形質転換体を用いて、NF- $\kappa$ Bの活性化を阻害または促進する物質をスクリーニングする方法、該スクリーニング用キット、該スクリーニング方法もしくはスクリーニング用キットを用いて得られるNF- $\kappa$ Bの活性化を阻害または促進する物質、該物質の製造方法、NF- $\kappa$ Bの活性化を阻害または促進する物質を含有している医薬などを提供する。

## 【 0 0 1 0 】

## 【課題を解決するための手段】

近年、生体内で発現している遺伝子を解析する手段として、cDNAの配列をランダムに解析する研究が活発に行われており、このようにして得られたcDNAの断片配列がEST (Expressed Sequence Tag、たとえば<http://www.ncbi.nlm.nih.gov/dbEST>) として、データベースに登録され公開されている。しかし、ESTは配列情報のみであり、その機能を推定することは困難である。また、ESTはUniGene (<http://www.ncbi.nlm.nih.gov/UniGene>) により整備され、これまでに約92000クラスターに登録されている。しかし、その多くは5'端ヌクレオチド配列を欠損しており、タンパク質翻訳開始部位を含まない。そのため、mRNAのコード領域の決定を前提とするタンパク質の機能解析、プロモーターの解析による遺伝子発現制御の理解といった遺伝子機能の解析に直結しているとは言いがたい。

## 【 0 0 1 1 】

一方、遺伝子の産物、すなわちタンパク質の機能を解明する方法の一つに、動物細胞を用いた一過性発現クローニング法がある（たとえば、実験医学別冊 遺伝子工学ハンドブック）。この方法は、動物細胞発現ベクターを用いて作製した cDNA ライブラリーを、動物細胞にトランスフェクションすることで機能的なタンパク質を直接発現させ、このタンパク質が細胞に及ぼす生物活性を指標として cDNA を同定、クローニングする方法である。この方法では、目的とするタンパク質産物に関する化学的情報（アミノ酸配列や分子量）をあらかじめ必要とせず、細胞内や培養液中に発現しているタンパク質の特異的生物活性を検出して cDNA クローンの同定を行うことができる。

## 【 0 0 1 2 】

この発現クローニングを効率良く行なうためには、cDNA ライブラリーの作製方法を工夫する必要がある。なぜなら、従来より汎用されている cDNA ライブラリー作製方法には幾つかの方法があるが（たとえば G u b b l e r - H o f f m a n の方法 : G e n e 2 5 ( 1 9 8 3 ) オカヤマーバーグの方法 : M o l . C e l l . B i o l . 2 ( 1 9 8 2 ) ）、これらの方法によって作製された cDNA は、そのほとんどが 5' 末端ヌクレオチド配列を欠損したものであり、完全長（mRNA の全ヌクレオチド配列を含む）であることは稀であるからである。その理由は、mRNA から cDNA を作るのに使用する逆転写酵素が、完全長の cDNA を作る効率が必ずしも高くないからである。

## 【 0 0 1 3 】

さらに、遺伝子の機能解析を試みるに際しては、完全長 cDNA をクローニングし、そこからタンパク質を発現させることが必須の要件である。従って、全体のクローンの中で、完全長のものの割合が高いライブラリーを作製することが、発現クローニングを効率良く行なうために必要であった。

## 【 0 0 1 4 】

本発明者らは、上記課題を解決するために鋭意研究を重ねた結果、オリゴキャッピング法を用いて完全長 cDNA ライブラリーを作製し、293EBNA 細胞を用いたアッセイ系を完成し、該アッセイ系により NF- $\kappa$ B を活性化する作用を有するタンパク質をコードする新規 DNA（cDNA）を単離することに成功

した。この新規DNAは、293EBNA細胞内で発現させることによりNF- $\kappa$ Bの活性化を誘発した。この結果は、この新規DNAがNF- $\kappa$ Bの活性化に関与するシグナル伝達分子であることを示しており、本発明を完成するに至った。

【0015】

すなわち、本発明は

(1) 以下の(a)または(b)の精製され、かつ単離されたタンパク質。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178において1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質。

【0016】



(2) 上記(1)記載のタンパク質とその全長にわたり少なくとも95%のアミノ酸配列の同一性を有するタンパク質であり、かつNF- $\kappa$ Bを活性化する作用を有する、精製されかつ単離されたタンパク質。

【0017】

(3) 以下の(a)または(b)のタンパク質をコードするヌクレオチド配列を包含する、単離されたポリヌクレオチド。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178において1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質。

【0018】

(4) 以下の(a)～(c)のいずれかのポリヌクレオチド配列を含む単離さ

れたポリヌクレオチド。

(a) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177で表されるポリヌクレオチド配列および該ポリヌクレオチド配列に相補的なポリヌクレオチド配列。

(b) (a) のポリヌクレオチド配列を有するポリヌクレオチドとストリンジェントな条件下でハイブリダイズし、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

(c) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177において、1若しくは複数個のヌクレオチド配列が欠失、置換若しくは付加されたポリヌクレオチド配列からなり、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

【0019】

(5) 上記(3)記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコー



ドするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

(6) 上記(4)記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

(7) 上記(3)～(6)のいずれか1つに記載のポリヌクレオチドによりコードされる精製されかつ単離されたタンパク質。

(8) 上記(3)～(6)のいずれか1つに記載のポリヌクレオチドを含有する組換えベクター。

(9) 上記(8)に記載の組換えベクターを含む形質転換された細胞。

(10) 上記(1)または(2)に記載のタンパク質が膜タンパク質である場合における、上記(9)記載の細胞の膜。

【0020】

(11) (a) 上記(3)～(6)のいずれか1つに記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

(b) 培地からタンパク質を回収する、  
ことを含む、タンパク質の製造方法。

【0021】

(12) (a) 個体のゲノムにおける上記(1)、(2)または(7)に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および/または

(b) 該個体に由来するサンプル中での該タンパク質の発現量を分析する、  
ことを含む該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、発現するタンパク質の量が正常の2倍以上の場合あるいは1/2以下の場合に病気であると診断する方法。

【0022】

(13) 以下の工程を含むNF- $\kappa$ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

(a) NF- $\kappa$ B を活性化するタンパク質をコードする遺伝子およびNF- $\kappa$ B の活性化に対応した、検出可能シグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

(c) 該形質転換された細胞と 1 あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、および

(e) 該検出可能なシグナルを正常より 2 倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを 2 分の 1 以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程。

【 0 0 2 3 】

(1 4) 以下の工程を含む、医薬組成物を製造する方法。

(a) NF- $\kappa$ B を活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

(c) 該形質転換された宿主細胞と 1 あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルを正常より 2 倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを 2 分の 1 以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程、および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

【 0 0 2 4 】

(1 5) NF- $\kappa$ B 活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

(a) NF- $\kappa$ B を活性化するタンパク質をコードする遺伝子、およびNF- $\kappa$

Bの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

(b) 検出可能なシグナルを測定するための試薬を含むキット。

【 0 0 2 5 】

(16) 上記(1)、(2)または(7)に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

(17) 上記(1)、(2)または(7)に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、上記(1)、(2)または(7)に記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

(18) NF- $\kappa$ Bの活性化タンパク質の発現を阻害する、上記(3)～(6)のいずれか1つに記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

(19) 上記(1)、(2)または(7)に記載のタンパク質をコードするRNAの開裂、またはI $\kappa$ Bの分解へ導く経路のタンパク質をコードするRNAの開裂により、NF- $\kappa$ Bの活性化を阻害するリボザイム。

【 0 0 2 6 】

(20) 炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される疾患の治療に有効な量の上記(13)に記載の方法でスクリーニングされた化合物および/または上記(16)に記載のモノクローナルまたはポリクローナル抗体および/または上記(18)に記載のアンチセンスオリゴヌクレオチドおよび/または上記(19)に記載のリボザイムを個体に投与することを含む疾患の治療法。

(21) NF- $\kappa$ Bの活性化を阻害または活性化するものとして上記(14)に記載の方法により製造された医薬組成物。

(22) 炎症、自己免疫疾患、癌およびウイルス性感染の治療のための上記(21)に記載の医薬組成物。

(23) NF- $\kappa$ B活性化を患っている患者に上記(14)に記載の方法により製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌およびウ

ウイルス感染を治療する方法。

(24) GVHD、Toxic epidermal necrolysis (TEN) などの皮膚疾患、IgA腎炎、紫斑病性腎炎、ループス腎炎などの増殖性腎炎および劇症肝炎の治療のための上記(21)記載の医薬組成物。

【0027】

(25) NF- $\kappa$ Bの阻害を患っている患者に上記(14)記載の方法により製造された医薬組成物を投与することからなるGVHD、Toxic epidermal necrolysis (TEN) などの皮膚疾患、IgA腎炎、紫斑病性腎炎、ループス腎炎などの増殖性腎炎および劇症肝炎を治療する方法。

(26) 上記(16)記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

(27) 上記(18)記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

(28) 対象疾患が炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される、上記(26)または(27)に記載の医薬組成物。

【0028】

(29) 機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

- (a) オリゴキャッピング法を用いて完全長cDNAライブラリーを作製し、
- (b) 完全長cDNAおよび該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに
- (c) シグナルを発するプラスミドを選択する。

【0029】

(30) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、

132、134、136、138、140、142、144、146、148、  
 150、151、153、155、157、159、161、163、165、  
 167、169、171、173、175および177で表されるヌクレオチド  
 配列のうち少なくとも1以上を含むデータセットおよび／または配列番号1、3  
 、5、7、9、11、13、15、17、19、21、23、25、27、29  
 、31、33、35、37、39、41、43、45、47、49、51、53  
 、55、57、59、61、63、65、67、69、71、73、75、77  
 、79、81、83、85、87、89、91、93、95、97、99、10  
 1、103、105、107、109、111、113、115、117、11  
 9、121、123、125、127、129、131、133、135、13  
 7、139、141、143、145、147、149、152、154、15  
 6、158、160、162、164、166、168、170、172、17  
 4、176および178で表されるアミノ酸配列のうち少なくとも1以上を含む  
 データセットを保存したコンピュータ読み込み可能媒体。

【0030】

(31) 上記(30)に記載の媒体上のデータと他のヌクレオチド配列および／  
 または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／  
 またはアミノ酸配列との同一性の算出を行う方法。

【0031】

(32) 配列番号2、4、6、8、10、12、14、16、18、20、2  
 2、24、26、28、30、32、34、36、38、40、42、44、4  
 6、48、50、52、54、56、58、60、62、64、66、68、7  
 0、72、74、76、78、80、82、84、86、88、90、92、9  
 4、96、98、100、102、104、106、108、110、112、  
 114、116、118、120、122、124、126、128、130、  
 132、134、136、138、140、142、144、146、148、  
 150、151、153、155、157、159、161、163、165、  
 167、169、171、173、175または177から選択されるヌクレオ  
 チド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質

## 【 0 0 3 2 】

( 3 3 ) 配列番号 1、 3、 5、 7、 9、 1 1、 1 3、 1 5、 1 7、 1 9、 2 1、 2 3、 2 5、 2 7、 2 9、 3 1、 3 3、 3 5、 3 7、 3 9、 4 1、 4 3、 4 5、 4 7、 4 9、 5 1、 5 3、 5 5、 5 7、 5 9、 6 1、 6 3、 6 5、 6 7、 6 9、 7 1、 7 3、 7 5、 7 7、 7 9、 8 1、 8 3、 8 5、 8 7、 8 9、 9 1、 9 3、 9 5、 9 7、 9 9、 1 0 1、 1 0 3、 1 0 5、 1 0 7、 1 0 9、 1 1 1、 1 1 3、 1 1 5、 1 1 7、 1 1 9、 1 2 1、 1 2 3、 1 2 5、 1 2 7、 1 2 9、 1 3 1、 1 3 3、 1 3 5、 1 3 7、 1 3 9、 1 4 1、 1 4 3、 1 4 5、 1 4 7、 1 4 9、 1 5 2、 1 5 4、 1 5 6、 1 5 8、 1 6 0、 1 6 2、 1 6 4、 1 6 6、 1 6 8、 1 7 0、 1 7 2、 1 7 4、 1 7 6 または 1 7 8 で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

## 【 0 0 3 3 】

まず、本発明の基本的特徴を更に明らかにするために、本発明の完成に至る経緯を追いながら、本発明について説明する。NF- $\kappa$ B を活性化する作用を有する新規遺伝子を取得する目的で、実施例に示すように、以下の実験を実行した。まずヒト正常肺線維芽細胞（三光純薬株式会社より購入）より調製した mRNA より、オリゴキャッピング法によって完全長 cDNA を作製し、該 cDNA をベクター pME18S-FL3 (GenBank Accession AB009864) に組み込んだ完全長 cDNA ライブラリーを作製した。次に、該 cDNA ライブラリーを大腸菌に導入し、1 クローンずつプラスミドを調製した。次に、293-EBNA 細胞（インビトロジェン社）に、ルシフェラーゼをコードする DNA を含有する pNF $\kappa$ B-Luc レポータープラスミド (STRATAGENE 社) と上記の完全長 cDNA プラスミドとを共導入した。そして、24 時間あるいは 48 時間培養後、ルシフェラーゼ活性を測定し、ルシフェラーゼ活性が対照実験（完全長 cDNA の代わりに、ベクター pME18S-FL3 を入れた細胞）と比べて有意に上昇している（対照実験と比べてルシフェラーゼ活性が 10 倍以上の値を示した）プラスミドを選抜し、該プラスミドにクローニングされている cDNA の全ヌクレ



オチド配列を決定した。このようにして得られた cDNA によりコードされるタンパク質は、該タンパク質が NF- $\kappa$ B の活性化に関与するシグナル伝達分子であることを示している。

次に、以下に本発明について詳細に説明する。

【 0 0 3 4 】

配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 のアミノ酸配列に関連して、本発明は、以下のタンパク質を提供する。

- (a) 上記アミノ酸配列を含むタンパク質。
- (b) 上記アミノ酸配列の 1 つを有するペプチド。
- (c) NF- $\kappa$ B を活性化し、かつ上記アミノ酸配列において、1 以上のアミノ酸の削除、置換または付加を有するタンパク質。
- (d) その全長にわたり配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 のアミノ酸配列に少なくとも 95%、好ましくは 97~99% の同一性を有するアミノ酸配列を

含むタンパク質。

【 0 0 3 5 】

“同一性”とは、当該技術で知られているとおり、配列を比較することにより決定される、2以上のタンパク質あるいは2以上のポリヌクレオチドの間の関係である。当該技術で“同一性”とは、タンパク質またはポリヌクレオチド配列の間の適合によって、あるいは場合によっては、一続きのそのような配列間の適合によって決定されるような、タンパク質またはポリヌクレオチド配列の間の配列相関性の程度を意味する。“同一性”および“類似性”は、既知の方法により容易に決定できる。同一性を決定する好ましい方法は、試験する配列間で最も長く適合するように設計される。同一性および類似性を決定するための方法は、公に利用可能なプログラムにコードされている。相同性決定には、AltschulらによるBLAST (Basic Local Alignment Search Tool) プログラム（たとえば、Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschyl SF, Madden TL, Schaffer AA, Zhang J, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997))を利用し決定することができる。

【 0 0 3 6 】

上記した配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178に記載されたアミノ酸配列からなるタンパク質がNF- $\kappa$ Bを活性化する作用を有することは、本願明細書実施例に記載の通りである。

【 0 0 3 7 】



配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177のポリヌクレオチドに関連して、本発明は、また以下の単離されたポリヌクレオチドを提供する。

(a) 上記配列に少なくとも95%、好ましくは97-99%の同一性を有するヌクレオチド配列を含むポリヌクレオチド。

(b) 上記配列のポリヌクレオチド。

(c) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178のアミノ酸配列に少なくとも95%、好ましくは97-99%の同一性を有するアミノ酸配列を有するタンパク質をコードするヌクレオチド配列を有するポリヌクレオチド。

【0038】

上記ヌクレオチド配列に含まれるヌクレオチド配列に同一またはほとんど同一なポリヌクレオチドは、本発明のタンパク質をコードする全長 cDNA 及びゲノムクローンまたは上記配列に対応する相同性の高い他の遺伝子の cDNA またはゲノムクローンを単離するためのハイブリダイゼーションプローブとして、また

は核酸増幅反応のためのプライマーとして使用してもよい。代表的には、これらのヌクレオチド配列は、上記配列に 70% 同一であり、好ましくは、80% 同一であり、より好ましくは 90% 同一であり、最も好ましくは、95% 同一である。プローブまたはプライマーは、一般的には少なくとも 15 ヌクレオチドを含有し、好ましくは 30 ヌクレオチドを含有し、50 ヌクレオチドを含有してもよい。特に好ましいプローブは、30～50 ヌクレオチドを有する。特に好ましいプライマーは、20～25 ヌクレオチドを有する。

## 【 0 0 3 9 】

本発明のポリヌクレオチドは、DNA の形態（たとえば、cDNA およびクローニングによって得られるか、あるいは合成的に生成されるゲノム DNA を含む）であってもよく、RNA（たとえば mRNA）の形態であってもよい。該ポリヌクレオチドは、二本鎖であっても、一本鎖であってもよい。二本鎖の場合は、二本鎖 DNA、二本鎖 RNA または DNA : RNA のハイブリッドであってもよい。一本鎖の場合は、センス鎖（コード鎖としても知られる）であっても、アンチセンス鎖（非コード鎖としても知られる）であってもよい。

## 【 0 0 4 0 】

当業者であれば、公知の方法を用いてこのタンパク質中のアミノ酸の置換などを適宜行い、配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 に記載のアミノ酸配列を有するタンパク質と同様に NF- $\kappa$ B を活性化する作用を有するタンパク質を作製することが可能である。一つの方法としては、該タンパク質をコードする DNA に対して、慣用の突然変異誘発法を使用する方法がある。別の方法としてはたとえば

部位特異的変異法（たとえば宝酒造株式会社のM u t a n - S u p e r E x p r e s s K m キット）が挙げられる。また、タンパク質のアミノ酸の変異は自然界においても生じうる。このようにアミノ酸の欠失、置換、付加により配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178のタンパク質に対してアミノ酸配列が変異した変異体であって、NF- $\kappa$ Bを活性化する作用を有するタンパク質及び該タンパク質をコードするDNAも本発明に含まれる。変異の数は、好ましくは10まで、より好ましくは5まで、最も好ましくは3までが好ましい。

## 【0041】

アミノ酸置換の例としては、保存的置換が好ましく、具体的には以下のグループ内での置換が挙げられる。（グリシン、アラニン）（バリン、イソロイシン、ロイシン）（アスパラギン酸、グルタミン酸）（アスパラギン、グルタミン）（セリン、トレオニン）（リジン、アルギニン）（フェニルアラニン、チロシン）。

## 【0042】

当業者であれば、ハイブリダイゼーション技術などを用いて配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137

、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質をコードするDNA（たとえば配列番号2）またはその一部を基に、これと類似性の高いDNAを単離して、該DNAから配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質と同様にNF- $\kappa$ Bを活性化する作用を有するタンパク質を得ることも通常行い得ることである。このように上記した配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列のタンパク質と高い同一性を有するタンパク質であって、NF- $\kappa$ Bを活性化する作用を有するタンパク質も本発明のタンパク質に含まれる。高い同一性とは、上記配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、

81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178であらわされるアミノ酸配列の全長にわたり少なくとも90%、好ましくは、少なくとも97-99%の同一性を有するアミノ酸配列を示す。

## 【0043】

本発明のタンパク質としては、ヒトや哺乳動物のあらゆる細胞や組織に由来する天然のタンパク質でもよく、化学合成タンパク質であってもよく、また遺伝子組換え技術によって得られたタンパク質でもよい。タンパク質は糖鎖やリン酸化などの翻訳後修飾は受けていても受けていなくても良い。

## 【0044】

本発明は、上記で示される本発明のタンパク質をコードするポリヌクレオチドである。上記の配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列としてより具体的には、たとえば配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114

、 1 1 6、 1 1 8、 1 2 0、 1 2 2、 1 2 4、 1 2 6、 1 2 8、 1 3 0、 1 3 2、 1 3 4、 1 3 6、 1 3 8、 1 4 0、 1 4 2、 1 4 4、 1 4 6、 1 4 8、 1 5 0、 1 5 1、 1 5 3、 1 5 5、 1 5 7、 1 5 9、 1 6 1、 1 6 3、 1 6 5、 1 6 7、 1 6 9、 1 7 1、 1 7 3、 1 7 5または1 7 7で表されるヌクレオチド配列が挙げられる。DNAはcDNAのほか、ゲノムDNA、化学合成DNAも含まれる。遺伝暗号の縮重に従い、遺伝子から生産されるタンパク質のアミノ酸配列を変えることなく配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列の少なくとも1つのヌクレオチドを他の種類のヌクレオチドに置換することができる。従って、本発明のDNAはまた、遺伝暗号の縮重に基づく置換によって変換されたヌクレオチド配列も含有する。このようなDNAは、公知の方法により合成することができる。

## 【 0 0 4 5 】

本発明のDNAは、配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177で表されるヌ



クレオチド配列からなるDNAとストリンジェントな条件下でハイブリダイズし、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするDNAも含まれる。ストリンジェントな条件とは、当業者には十分理解できることであり、たとえば、T. Maniatisらの実験操作書(Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory 1982、1989)に従えば容易に実施できる。

## 【 0 0 4 6 】

すなわち、ストリンジェントな条件とは、30%ホルムアミドを含むハイブリダイゼーション溶液中(5×SSC(0.75MのNaCl、75mMのクエン酸三ナトリウム)、5×デンハルト溶液、0.5%SDS、100 $\mu$ g/mlの変性せん断サケ精子DNA)で37℃のインキュベーションを一晩行い、その後2×SSC、0.1%SDS中、室温で10分の洗浄を3回行い、次いで1×SSC、0.1%SDS中、37℃で10分の洗浄を2回行う条件である(低ストリンジェンシー)。より好ましい条件は、40%ホルムアミドを含むハイブリダイゼーション溶液中で42℃のインキュベーションを一晩行い、その後2×SSC、0.1%SDS中、室温で10分の洗浄を3回行い、次いで0.2×SSC、1%SDS中、42℃で10分の洗浄を2回行う条件である(中ストリンジェンシー)。最も好ましい条件は、50%ホルムアミドを含むハイブリダイゼーション溶液中で42℃のインキュベーションを一晩行い、その後2×SSC、0.1%SDS中、室温で10分の洗浄を3回行い、次いで0.2×SSC、0.1%SDS中、50℃で10分の洗浄を2回行う条件である(高ストリンジェンシー)。この際、得られたDNAは、NF- $\kappa$ Bを活性化する作用を有するタンパク質をコードすることが必須である。

## 【 0 0 4 7 】

本発明は、上記(3)あるいは(4)のポリヌクレオチドのヌクレオチド配列と高い類似性を有し、かつNF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするヌクレオチドを含むポリヌクレオチドを含む。代表的には、これらのヌクレオチド配列は、上記(3)または(4)のポリヌクレオチドのヌクレオチド配列

の全長にわたり 9 5 % 同一であり、より好ましくは 9 7 % 同一であり、最も好ましくは少なくとも 9 9 % 同一である。

【 0 0 4 8 】

上記の本発明の DNA は、前述のタンパク質を、組換え DNA 技術を用いて製造するのに用いることができる。本発明の DNA 及びペプチドは、概略以下のようにして得ることができる。

(A) 本発明のタンパク質をコードする DNA をクローニングする。

(B) タンパク質の全コード領域あるいはその一部をコードする DNA を発現用ベクターに組み込んで、組換えベクターを構築する。

(C) 構築した組換えベクターにより、宿主細胞を形質転換する。

(D) 得られた細胞を培養し、該タンパク質、またはその類縁体を発現させ、カラムクロマトグラフィーにより精製する。

【 0 0 4 9 】

上記の工程中で DNA、組換え体宿主としての大腸菌等の取り扱いに必要な一般的な操作は、当業者間で通常行われているものであり、たとえば、上記 T. Maniatis らの実験操作書に従えば容易に実施できる。使用する酵素、試薬類も全て市販の製品を用いることができ、特に断らない限り、製品で指定されている使用条件に従えば、完全にそれらの目的を達成することができる。以下に上記 (A) ~ (D) の工程について更に詳しく説明する。

【 0 0 5 0 】

上記 (A) における本発明のタンパク質をコードする DNA のクローニングの手段としては、本願明細書実施例に記載した方法の他に、本発明のヌクレオチド配列（たとえば配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、14



8、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177)の一部を有する合成DNAをプライマーとしたPCR法によって増幅する方法、あるいは、適当なベクターに組み込んだDNAを本発明のタンパク質の一部あるいは全領域をコードするDNA断片もしくは合成DNAを標識したものとのハイブリダイゼーションによって選別すること、などが挙げられる。細胞、組織より全RNAまたはmRNA画分を調製したものをを用いて直接Reverse Transcriptase Polymerase Chain Reaction (RT-PCR法)によって増幅することもできる。適当なベクターに組み込んだDNAとしては、たとえば市販されている (CLONTECH社、STRATAGENE社) ライブラリーを使用することができる。ハイブリダイゼーションの方法は、当業者間で通常行われているものであり、たとえば、上記T. Maniatisらの実験操作書に従えば容易に実施できる。クローン化された本発明のタンパク質をコードするDNAは目的によりそのまま、または所望により制限酵素で消化したり、リンカーを付加したりして使用することができる。上記のようにして得られるDNAは、配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177に記載のヌクレオチド配列を有する遺伝子であるか、あるいは前述の(3)～(6)のポリヌクレオチドであればよい。上記(B)において発現ベクターに組み込むDNAは、上述のタンパク質の全長をコードする全長cDNAでも、DNA断片でも良いし、その一部分を発現する様に構築されたDNA断片でも良い。

すなわち、本発明は、上記のDNAを含有する組換えベクターである。

## 【 0 0 5 1 】

本発明のタンパク質の発現ベクターは、たとえば、本発明のタンパク質をコードするDNAから目的とするDNA断片を切り出し、該DNA断片を適当な発現ベクター中のプロモーターの下流に連結することにより製造することができる。

## 【 0 0 5 2 】

用いる発現ベクターとしては、複製可能であれば、大腸菌をはじめとする原核生物由来、酵母由来、真菌由来、昆虫ウイルス由来、脊椎動物ウイルス由来いずれのベクターでも良いが、宿主として使用する微生物または細胞に適したものを選択する必要がある。また、発現物に応じて、宿主細胞－発現ベクター系としては、適切な組み合わせが選択される。

微生物を宿主として使用する場合、これら微生物に適したプラスミドベクターが組み換え体DNAの複製可能な発現ベクターとして一般に用いられる。

## 【 0 0 5 3 】

たとえば、大腸菌を形質転換するためのプラスミドベクターとしては、プラスミドpBR322やpBR327などを用いることができる。プラスミドベクターは通常複製起源、プロモーター、及び組換え体DNAで形質転換した細胞を選別するのに有用な表現型を組換え体DNAに与えるマーカー遺伝子等を含んでいる。プロモーターの例としては、 $\beta$ -ラクタマーゼプロモーター、ラクトースプロモーター、トリプトファンプロモーター等が挙げられる。マーカー遺伝子の例としては、アンピシリン耐性遺伝子やテトラサイクリン遺伝子などが挙げられる。適した発現ベクターの例としては、プラスミドpBR322、pBR327の他に、pUC18、pUC19等が挙げられる。

## 【 0 0 5 4 】

酵母で本発明のDNAを発現するためには、複製可能なベクターとして、たとえばYEp24を用いることができる。プラスミドYEp24はURA3遺伝子を含含有しており、このURA3遺伝子をマーカー遺伝子として利用することができる。酵母細胞用の発現ベクターのプロモーターの例としては、3-ホスホグリセレートキナーゼ、グリセルアルデヒド-3-ホスフェートデヒドロゲナーゼ、アルコールデヒドロゲナーゼなどの遺伝子のプロモーター等が挙げられる。

## 【 0 0 5 5 】

真菌で本発明のDNAを発現するための発現ベクターに用いられるプロモーター及びターミナーターの例としては、ホスホグリセレートキナーゼ (PGK)、グリセルアルデヒド-3-ホスフェートデヒドロゲナーゼ (GAPD)、アクチン等の遺伝子プロモーター及びターミネーターが挙げられる。適した発現ベクターの例としては、プラスミド pPGACY2、pBSFAHY83等が挙げられる。

## 【 0 0 5 6 】

昆虫細胞で本発明のDNAを発現させるための発現ベクターに用いられるプロモーターの例としては、ポリヘドリンプロモーター、P10プロモーターなどが挙げられる。

## 【 0 0 5 7 】

動物細胞で本発明のDNAを発現させるための組換えベクターは、一般に遺伝子を制御するための機能配列、たとえば、複製起源、本発明のDNAの上流に位置すべきプロモーター、リボソーム結合部位、ポリアデニル化部位や転写終止配列を含有している。本発明のDNAを真核細胞内で発現させるのに用いることができるそのような機能配列はウイルスやウイルス性物質から得ることができる。例えば、SR $\alpha$ プロモーター、SV40プロモーター、LTRプロモーター、CMV (サイトメガロウイルス) プロモーター、HSV-TKプロモーターなどがあげられる。これらのうち、CMVプロモーター、SR $\alpha$ プロモーターなどを用いるのが好ましい。また、本発明のタンパク質をコードする遺伝子の上流位置に本来存在するプロモーターも、上述の宿主ベクター系で使用するのに適しているならば使用することができる。複製起源については、外来性の起源、たとえばアデノウイルス、ポリオーマ、SV40等のウイルス由来の複製起点を用いることができる。また、発現ベクターとして宿主染色体に組み込まれるような性質を有するベクターを用いる場合、宿主染色体の複製起源を利用することができる。適した発現ベクターの例としては、プラスミド pSV-dhfr (ATCC 37146)、pBPV-1 (9-1) (ATCC 37111)、pcDNA3.1 (INVITROGEN社)、pME18S-FL3等が挙げられる。

## 【 0 0 5 8 】

本発明は、上記の組換えベクターを含む形質転換された細胞である。本発明の複製可能な組換えベクターで形質転換された微生物または細胞は、前述の通り、組換えベクターに与えられた少なくとも1種の表現型によって形質転換されずに残った親細胞から選別される。表現型は少なくとも1種のマーカー遺伝子を組換えベクターに挿入することによって与えることができる。また複製可能なベクターが本来有しているマーカー遺伝子を利用することもできる。マーカー遺伝子の例としては、たとえば、ネオマイシン耐性などの薬剤耐性遺伝子やジヒドロ葉酸レダクターゼをコードする遺伝子などが挙げられる。

## 【 0 0 5 9 】

上記 (C) において用いる宿主としては、大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良いが、用いる発現ベクターに適したものを選択する必要がある。微生物の例としては、エシュリヒア コリ (*Escherichia coli*) の菌株、たとえば *E. coli* K12 株 294 (ATCC 31446)、*E. coli* X1776 (ATCC 31537)、*E. coli* C600、*E. coli* JM109、*E. coli* B 株、あるいはバチラス サブチリス (*Bacillus subtilis*) の如き *Bacillus* 属の菌株、あるいはサルモネラ チフィムリウム (*Salmonella typhimurium*) またはセラチア マーゼサンス (*Serratia marcesans*) 等の大腸菌以外の腸内菌、あるいはシュードモナス (*Pseudomonas*) 属の種々の菌株が挙げられる。酵母としては、たとえば、サッカロミセス セレビシエ (*Saccharomyces cerevisiae*)、シゾサッカロマイセス ポンベ (*Schizosaccharomyces pombe*)、ピキア パストリス (*Pichia pastoris*) などが用いられる。真菌としては、たとえば、アスペルギルス ニドランス (*Aspergillus nidulans*)、アクレモニウム クリソゲナム (*Acremonium chrysogenum*) (ATCC 11550) 等が挙げられる。

## 【 0 0 6 0 】

昆虫細胞としては、たとえば、ウイルスがA c N P Vの場合は、夜盗蛾の幼虫由来株化細胞 (S p o d o p t e r a f r u g i p e r d a : S f細胞)、T r i c h o p l u s i a n iの卵由来のH i g h F i v e T M細胞、などが用いられる。動物細胞の例としては、H E K 2 9 3細胞、C O S - 1細胞、C O S - 7細胞、H e l a細胞、チャイニーズハムスター (C H O)細胞等が挙げられる。これらの中でも、C H O細胞およびH E K 2 9 3細胞が好ましい。細胞を宿主とする場合、用いられる発現ベクターと宿主細胞の組合せは実験の目的により異なるが、その組合せにより、一過的発現、構成的発現の2種類の発現方式が考えられる。

## 【 0 0 6 1 】

上記 (C) における微生物及び細胞の形質転換とは、D N Aを強制的な方法や、細胞の貪食能により微生物や細胞に取り込ませ、プラスミド状態あるいは染色体に組み込まれた状態でD N Aの形質を一過的あるいは構成的に発現させることである。当業者であれば公知の方法によって形質転換できる (たとえば実験医学別冊遺伝子工学ハンドブック)。たとえば動物細胞の場合、D E A E - デキストラン法、リン酸カルシウム法、エレクトロポレーション法 (電気穿孔法)、リポフェクション法などの方法でD N Aを細胞に導入することができる。動物細胞を用いて、本発明のタンパク質を安定に発現させる方法としては、上記の動物細胞に導入された発現ベクターが染色体に組み込まれた細胞をクローン選択によって選択する方法がある。具体的には、上記の選択マーカーを指標にして形質転換体を選択する。さらに、このように選択マーカーを用いて得られた動物細胞に対して、繰り返しクローン選択を行なうことにより本発明のタンパク質の高発現能を有する安定な動物細胞株を得ることができる。また、D i h y d r o f o r a t e r e d u c t a s e (D H F R) 遺伝子を選択マーカーとして用いた場合M e t h o t r e x a t e (M T X) 濃度を徐々に上げて培養し、耐性株を選択することにより、D H F R遺伝子とともに、本発明のタンパク質をコードするD N Aを細胞内で増幅させて、さらに高発現の動物細胞株を得ることもできる。

## 【 0 0 6 2 】

上記の形質転換された細胞を本発明のタンパク質をコードするD N Aが発現可



能な条件下で培養し、本発明のタンパク質を生成、蓄積せしめることによって、本発明のタンパク質を製造することができる。すなわち、本発明は、上記（３）～（６）に記載の単離されたポリヌクレオチドを含む形質転換された細胞を、該ポリヌクレオチドによりコードされているタンパク質を発現させる条件下培養し、次いで培地から該タンパク質を回収することを含む該タンパク質の製造方法である。

## 【 0 0 6 3 】

上記の形質転換された細胞の培養は、当業者に公知の方法で行なうことができる（たとえばバイオマニュアルシリーズ４、羊土社）。たとえば動物細胞の場合、各種の動物細胞培養法、たとえば、シャーレ培養、マルチトレイ式培養、モジュール培養などの付着培養、または細胞培養用担体（マイクロキャリアー）に付着させるか生産細胞自体を浮遊化させ浮遊培養等の公知の方法により培養を行なえば良い。培地は通常良く用いられる動物細胞用の培地、たとえばD-MEMやRPMI 1640等を用いれば良い。

## 【 0 0 6 4 】

上記培養物から本発明のタンパク質を分離精製するには、自体公知の分離・精製法を適切に組み合わせて行なうことができる。これらの公知の分離、精製法としては、塩析や溶媒沈澱法などの溶解度を利用する方法、イオン交換クロマトグラフィーなどの荷電の差を利用する方法、透析法、限外ろ過法、ゲルろ過法、およびSDS-ポリアクリルアミドゲル電気泳動法などの主として分子量の差を利用する方法、アフィニティークロマトグラフィーなどの特異的親和性を利用する方法、逆相高速液体クロマトグラフィーなどの疎水性の差を利用する方法、等電点電気泳動法などの等電点の差を利用する方法などが用いられる。たとえば、本発明のタンパク質は、硫酸またはエタノール沈殿、酸抽出、アニオンまたはカチオン交換クロマトグラフィー、ホスフォセルロースクロマトグラフィー、疎水性相互作用クロマトグラフィー、アフィニティークロマトグラフィー、ヒドロキシアパタイトクロマトグラフィーおよびレクチンクロマトグラフィーを含む既知の方法により組換え細胞培養物から回収し、精製することができる。最も好ましくは、高性能液体クロマトグラフィーが精製に使用される。ポリペプチドが細胞内合



成、単離または精製の間に変性するときには、活性なコンフォーメーションを再生するためにタンパク質をリフォールディングするためのよく知られた技術を使用できる。

## 【 0 0 6 5 】

本発明のタンパク質を他のタンパク質との融合タンパク質として製造することができる。これらも、本発明に含まれる。この融合タンパク質を発現する際に用いられるベクターとしては、該タンパク質をコードするDNAを組み込むことができ、かつ該融合タンパク質を発現することができるベクターであれば、いかなるベクターでも用いることができる。本発明のペプチドに融合できるタンパク質としては、たとえばグルタチオン-S-トランスフェラーゼ (GST)、ヒスチジン残基の6個の連続配列 (6×His) 等が挙げられる。本発明のタンパク質を他の蛋白質と融合した蛋白質として発現させた場合には、融合した蛋白質に親和性をもつ物質を用いたアフィニティークロマトグラフィーを用いて精製することができ、有利である。例えば、GSTとの融合蛋白質として生産した場合は、グルタチオンをリガンドとするアフィニティークロマトグラフィーにより精製することができる。

## 【 0 0 6 6 】

本発明は、上記(7)のタンパク質の活性を阻害するタンパク質を含む。たとえば、抗体や上記(7)のタンパク質の活性中心等に結合し、活性の発現を妨げる他のタンパク質が挙げられる。

本発明は、前記の本発明のタンパク質あるいはその部分ペプチドに特異的に結合する抗体ならびにそのような抗体の製造方法に関する。抗体は、本発明のタンパク質を認識し得る抗体であれば、ポリクローナル抗体、モノクローナル抗体、ならびにこれらの抗体のフラグメント、一本鎖抗体、ヒト化抗体の何れであってもよい。抗体フラグメントは、公知の技術によって作製することができる。たとえば、該抗体フラグメントには、限定されるものではないが、F(a b') 2フラグメント、F a b' フラグメント、F a b フラグメント及びF v フラグメントが含まれる。たとえば、モノクローナル抗体またはポリクローナル抗体は、上記(1)または(2)に記載のタンパク質を抗原またはエピトープ含有フラグメン

トとして非ヒト動物に投与することにより得られる。本発明のタンパク質に対する抗体は、本発明のタンパク質あるいはそのペプチドを抗原として用い、自体公知の抗体または抗血清の製造法に従って製造することができる。たとえば実験医学別冊 新遺伝子工学ハンドブック 改訂第3版に記載の方法が挙げられる。

## 【 0 0 6 7 】

ポリクローナル抗体の場合であれば、たとえば、本発明のタンパク質をウサギなどの動物に本発明のタンパク質あるいはペプチドを注射することにより該タンパク質あるいはペプチドに対する抗体を産生させ、次いで血液を採取し、これを、たとえば硫酸沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

## 【 0 0 6 8 】

モノクローナル抗体の場合は、たとえば、本発明のタンパク質をマウスなどの動物に免疫し、同マウスから脾臓を抽出し、これをすりつぶして細胞にし、マウスミエローマ細胞とポリエチレングリコールなどの試薬により融合させ、これによりできた融合細胞（ハイブリドーマ）の中から、本発明のタンパク質に対する抗体を産生するクローンを選択する。次いで、得られたハイブリドーマをマウス腹腔内に移植し、同マウス内より腹水を回収し、得られたモノクローナル抗体を、たとえば硫酸沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

## 【 0 0 6 9 】

得られた抗体をヒトに投与する目的で使用する場合は、免疫原性を低下させるために、ヒト型化抗体あるいはヒト抗体を用いることが好ましい。ヒト型化抗体は、トランスジェニックマウスまたは他の哺乳動物を用いて作製することができる。これらのヒト型化抗体のやヒト抗体の一般的概説は、たとえば、M o r r i s o n, S. L. e t a l. [P r o c. N a t l. A c a d. S c i. U S A, 8 1 : 6 8 5 1 - 6 8 5 5 ( 1 9 8 4 ) ]、J o n e s, P. T. e t a l [N a t u r e 3 2 1 : 5 2 2 - 5 2 5 ( 1 9 8 6 ) ]、野口浩〔医学のあ

ゆみ 1 6 7 : 4 5 7 - 4 6 2 ( 1 9 9 3 ) ]、松本隆志 [ 化学と生物 3 6 : 4 4 8 - 4 5 6 ( 1 9 9 8 ) ] によって供されている。ヒト化キメラ抗体は、マウス抗体の V 領域とヒト抗体の C 領域を遺伝子組換えにより結合し、作製することができる。ヒト化抗体は、マウスのモノクローナル抗体から相補性決定部位 ( C D R ) 以外の領域をヒト抗体由来の配列に置換することによって作製できる。また、免疫系をヒトのものと入れ換えたマウスを用いて、該マウスを免疫して、通常のモノクローナル抗体と同様に直接ヒト抗体を作製することもできる。これらの抗体は、タンパク質を発現するクローンを単離したり同定するのに使用できる。また、これらの抗体は、本発明のタンパク質を細胞抽出液、または本発明のタンパク質を産生する形質転換細胞から精製するのに使用できる。更にこれらの抗体は、細胞や組織中の本発明のタンパク質を検出する E L I S A や R I A ( ラジオイムノアッセイ )、またはウエスタンブロット系の構築に使用できる。このような検出系は、動物、好ましくは、ヒトの組織または血管内流体などの身体サンプル中に存在する本発明のタンパク質の存在量を検出する診断目的に使用することができる。たとえば、これらの抗体は、炎症、自己免疫疾患、感染症 ( 一例として H I V 感染 )、癌などの、本発明のタンパク質の ( 発現 ) 異常に起因する H F -  $\kappa$  B の望ましくない活性化によって特徴付けられる疾患の診断に使用できる。疾患の診断の基礎を提供するために、本発明のタンパク質の発現についての通常の値、すなわち標準値が確立されなければならないが、これは当業者においては周知の技術である。すなわち、複合体形成のための適切な条件下で、ヒトあるいは動物のどちらでもよいが、正常の被験者から得られた体液あるいは細胞抽出物と、本発明のタンパク質に対する抗体とを結合させ、この抗体-タンパク複合体の量を化学的または物理的手段により検出し、これを既知量の抗原 ( 本発明のタンパク質 ) を含む標準液を用いて作成した標準曲線を用いて、正常サンプルから得られた標準値を算出する。標準値と本発明のタンパク質が関係する疾患を潜在的に患う被験者からのサンプルから得られた値と比較し、標準値との偏差によって疾病の存在を確認することができる。また、これらの抗体は、本発明のタンパク質の機能を研究する試薬としても用いることができる。

【 0 0 7 0 】

本発明の抗体は精製され得、次いで、たとえば、炎症、自己免疫疾患、感染症（一例としてH I V感染）、癌などの、本発明のタンパク質の（発現）異常に起因するH F -  $\kappa$  Bの望ましくない活性化によって特徴付けられる疾患の患者に投与され得る。すなわち本発明は、上記に記載の抗体を有効成分として含有する医薬、および抗体を用いた治療方法である。これらの医薬は治療的使用のためにさらなる有効成分または不活性成分（たとえば、従来の薬学的に受容可能なキャリアまたは希釈剤（たとえば、免疫原性アジュバント）と、生理学的に無毒の安定化剤および賦形剤とともに組み合わせられ得る。これらの組み合わせは、濾過滅菌され、そして凍結乾燥により投薬バイアル中に、または安定化水性調製物中の貯蔵物として投薬形態にされ得る。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射などの当業者に公知の方法により行い得る。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。これらの抗体は、本発明のタンパク質で仲介されるN F -  $\kappa$  Bの活性化を阻害し、治療効果を示す。

## 【 0 0 7 1 】

本発明のD N Aは、細胞内シグナリングプロセスに関与する他のタンパク質を単離、同定、クローン化することにも使用できる。たとえば、本発明のタンパク質をコードするD N A配列は、コードされたタンパク質を「バイト（b a i t）」として用いて、c D N AまたはゲノムD N Aライブラリーから、本発明のタンパク質に結合できるタンパク質をコードする他の配列「プレイ（p r e y）」を単離し、クローン化する酵母ツーハイブリッドシステム（たとえばN a t u r e、3 4 0 : 2 4 5 - 2 4 6（1 9 8 9））に用いることができる。同様の方式で、本発明のタンパク質が、他の細胞タンパク質（たとえばN I K, T R A F 2）に結合できるかどうかも決定することができる。あるいは別の方法として、本発明のタンパク質の抗体を用いた免疫沈降法（たとえば、実験医学別冊新遺伝子工学ハンドブック）によって、本発明のタンパク質に結合し得るタンパク質を細胞抽出物から単離する方法が挙げられる。さらに別の方法として、上記に記載のように、本発明のタンパク質を他のタンパク質との融合タンパク質として発現させ、融合タンパク質に対する抗体を用いて免疫沈降法を行ない、本発明のタンパク



質に結合し得るタンパク質を単離する方法が挙げられる。

【 0 0 7 2 】

診断アッセイは、前述の方法により、NF- $\kappa$ Bを活性化する機能を持つ（１）、（２）または（７）のタンパク質遺伝子中の変異を検出することにより疾患の診断や該疾患への感受性を決定するための方法を提供する。さらに、このような疾患は、個体に由来するサンプル中のタンパク質またはmRNAレベルの異常な減少または増加を測定することを含む方法によって診断してもよい。発現の減少または増加は、当該技術でRNAレベルでのポリヌクレオチドの定量によく知られた方法、たとえば、RT-PCRなどの核酸増幅法、およびRNase保護法、ノーザンブロット法その他のハイブリダイゼーション法などの方法で測定できる。宿主に由来するサンプル中のタンパク質レベルの測定に使用され得るアッセイ技術は、当業者によく知られている。そのような方法には、ラジオイムノアッセイ、競合的結合測定法、ウェスタンブロット分析およびELISAアッセイが含まれる。本発明のDNAは、本発明のタンパク質またはそのペプチドフラグメントをコードするDNAまたはmRNAにおける異常を検出するのに使用できる。本発明は、個体における上記（１）、（２）または（７）に記載のタンパク質の発現に関連した疾患または疾患への感受性を診断する方法に関する。該方法は、タンパク質をコードするポリヌクレオチド配列における変異を、測定することを含む。

【 0 0 7 3 】

本発明のDNAは、本発明のDNAを用いることによって、本発明のタンパク質またはその部分ペプチドをコードするDNAまたはmRNAの異常を検出することができるので、たとえば、該DNAまたはmRNAの損傷、突然変異あるいは発現低下や、増加あるいは発現過多などの遺伝子診断に有用である。すなわち本発明は、個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、

（a）個体のゲノムにおける請求項１または２に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

（b）該個体に由来するサンプル中での該タンパク質の発現量を分析する、こと

を含む診断方法であって、発現するタンパク質の量が正常の2倍以上あるいは1/2以下の場合に病気であると診断する方法に関する。

## 【 0 0 7 4 】

上記 (a) により、NF- $\kappa$ B を活性化する機能を持つ (1)、(2) または (7) のタンパク質をコードするヌクレオチド配列に変異がある場合は、該変異が NF- $\kappa$ B の活性化に関連した疾病を引き起こす可能性がある。あるいは、(b) により、被験者における前記 (1)、(2) または (7) のタンパク発現量を測定し正常値を異なる値を示す場合は、NF- $\kappa$ B を活性化する作用を持つ本発明の新規タンパク質の発現量異常が NF- $\kappa$ B の活性化に関連した疾病の原因である可能性がある。ここで、(a) の NF- $\kappa$ B を活性化する機能を持つ (1)、(2) または (7) のタンパク質をコードするヌクレオチド配列の変異の有無を測定する方法としては、それらのタンパク質遺伝子のヌクレオチド配列の一部をプライマーとして、RT-PCRを行い、その後通常のヌクレオチド配列決定方法によって配列を決定し、変異の有無を検出できる。あるいは、PCR-SSCP法 (Genomics, 5: 874-879, 1989年、実験医学別冊新遺伝子工学ハンドブック) によっても変異の有無を調べることができる。

## 【 0 0 7 5 】

また、(b) のタンパク発現量を調べる方法としては、たとえば、前記 (16) に記載の抗体を利用する方法が挙げられる。ヌクレオチド配列を決定する方法としては、たとえば、上記 (3) ~ (6) に記載の遺伝子のヌクレオチド配列の一部をプライマーとしてRT-PCRを行ない、その後通常のヌクレオチド配列決定方法によって配列を決定し変異の有無を検出できる。あるいはPCR-SSCP法 (Genomics, 5: 874-879, 1989年、実験医学別冊新遺伝子工学ハンドブック) によっても変異の有無を調べることができる。

また、本発明は、本発明のタンパク質によるNF- $\kappa$ B の活性化を阻害または促進する化合物のスクリーニング方法に関する。

## 【 0 0 7 6 】

このスクリーニング方法は、

(a) NF- $\kappa$ B を活性化する作用を有するタンパク質をコードする遺伝子およ



び検出可能なシグナルを提供し得る成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

(c) 該形質転換された細胞と 1 あるいは複数個の被検化合物とを接触させる工程、

(d) 検出可能なシグナルを検出する工程、および

(e) 該検出可能なシグナルを正常より 2 倍以上に増加させる化合物を活性化剤化合物として単離または同定し、また該検出可能なシグナルを 2 分の 1 以下に減少させる化合物を阻害剤化合物として単離または同定する工程、を含む。

#### 【 0 0 7 7 】

検出可能なシグナルを提供し得る成分としては、たとえばレポーター遺伝子が挙げられる。レポーター遺伝子は、テストを行なう転写因子の活性化を直接検出するかわりに用いられるもので、調べたい遺伝子のプロモーターをレポーター遺伝子につなぎ、レポーター遺伝子の産物の活性を測定することによってプロモーターの転写活性の解析を行なうものである（バイオマニュアルシリーズ 4、羊土社（1994））。

#### 【 0 0 7 8 】

レポーター遺伝子としては、その発現産物の活性または生産量（mRNA の生産量も含まれる）を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコールアセチルトランスフェラーゼ、 $\beta$ -ガラクトシダーゼ、ルシフェラーゼ等の酵素活性を測定することで利用できる。NF- $\kappa$ B の活性化を評価するのに用いるレポータープラスミドとしては、NF- $\kappa$ B 認識配列をレポーター遺伝子の上流に組み込んだものであればよく、たとえば pNF- $\kappa$ B-Luc（STRATAGENE 社）が利用できる。あるいは、Tanaka S. et. al J. Vet. Med. Sci. Vol. 59 (7)、Rothe M. et. al. Science Vol. 269 p1424-1427 (1995) に記載の NF- $\kappa$ B 依存レポータープラスミドが例示される。

## 【 0 0 7 9 】

宿主細胞としては、NF- $\kappa$ Bの活性化を検出し得る細胞であればよく、好ましくは、哺乳動物細胞であり、たとえば293EBNA細胞が好適に用いられる。形質転換及び培養に関しては、上記に記載の通りである。

## 【 0 0 8 0 】

NF- $\kappa$ Bの活性化を阻害または促進する化合物のスクリーニングは、具体的には、たとえば、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することにより、NF- $\kappa$ Bの活性化を阻害または促進する化合物をスクリーニングすることができる。レポーター活性の測定は、当業者に公知の方法（たとえばバイオマニユアルシリーズ4、羊土社（1994））で行なうことができる。スクリーニングの被検物質には特に制限はなく、低分子化合物、ペプチドなどが挙げられる。被検化合物は、人工的に合成したものであっても、天然に存在するものであっても良い。また単一物質でも、混合物でもい。検出可能なシグナルとしては、上記レポーター遺伝子の他に、NF- $\kappa$ Bの活性化によって発現が誘導されることが知られている、たとえばIL-1やTNF- $\alpha$ の遺伝子のmRNA量あるいはタンパク量を測定しても良い。mRNA量の測定は、たとえばノーザンハイブリダイゼーションやRT-PCR法などが挙げられる。タンパク量の測定はたとえば抗体を用いる方法が挙げられる。抗体は公知の方法によって作製しても良いし、市販のもの（たとえば和光純薬工業株式会社）を使用することもできる。

## 【 0 0 8 1 】

また、以下の（a）～（f）の工程により医薬組成物を製造することも可能である。

（a）NF- $\kappa$ Bを活性化する作用を有するタンパク質をコードする遺伝子および検出可能なシグナルを与えることができる成分を細胞に提供する工程、

（b）該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

（c）該形質転換された宿主細胞と1あるいは複数個の化合物とを接触させる工

程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルを正常より 2 倍以上に増加させる化合物を活性化剤化合物として単離または同定し、また該検出可能なシグナルを 2 分の 1 以下に減少させる化合物を阻害剤化合物として単離または同定する工程、および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

【 0 0 8 2 】

本願発明のタンパク質は、以下の工程により、該タンパク質のアゴニスト、アンタゴニストまたは阻害剤を、構造を基礎にして設計する方法に使用してもよい。

(a) まず、タンパク質の三次元構造を決定する工程、

(b) アゴニスト、アンタゴニストまたは阻害剤の反応性部位または結合部位と思われる部位の三次元構造を推論する工程、

(c) 推論した結合部位または反応性部位に結合するかあるいは結合すると予測される候補化合物を合成する工程、および

(d) 該候補化合物が本当にアゴニスト、アンタゴニストまたは阻害剤であるか否かを試験する工程。

【 0 0 8 3 】

また本発明は、上記スクリーニングによって得られた化合物を含む。しかしながら、本発明のスクリーニング方法は、上記の方法に限定されるものではない。さらに、上記 (14) に記載の方法により医薬組成物を製造する方法も含む。

【 0 0 8 4 】

該候補化合物には特に制限はなく、低分子化合物、ペプチドなどが挙げられ、また、人工的に合成したものであっても、天然に存在するものであっても良い。上記スクリーニングによって得られた化合物は、NF- $\kappa$ B の活性化を阻害または促進する作用を有しているので、NF- $\kappa$ B の望ましくない活性化あるいは不活性化に起因する疾患を治療または予防するための医薬として有用である。混合物から目的化合物を単離、精製するには、自体公知の方法、例えば濾過、抽出、洗浄、乾燥、濃縮、結晶化、各種クロマトグラフィー等を適宜組み合わせて行な

うことができる。化合物の塩を取得したい時は、化合物が塩の形で得られる場合にはそのまま精製すれば良く、また遊離の形で得られる場合には、通常の方法により適当な溶媒に溶解または懸濁し、所望の酸または塩基を添加し、塩を形成させて単離精製すれば良い。本発明の方法を用いて得られる化合物またはその塩を医薬組成物とする場合、常法により製剤化することができる。すなわち活性成分として有効な量の上記化合物またはその薬理的に許容される塩と、薬理的に許容される担体とを混合すれば良い。製剤化は選沢された投与様式に適した形態が選ばれる。経口投与に適した組成物としては、錠剤、顆粒剤、カプセル剤、丸剤、および散剤などの固体形態、溶液剤、シロップ剤、エリキシル剤、および懸濁液剤などの液体形態が挙げられる。非経口投与に有用な形態としては、無菌溶液剤、乳剤、および懸濁液剤が挙げられる。上記の担体としては、例えばゼラチン、乳糖、グルコース等の糖類、コーン・小麦・米・とうもろこし澱粉等の澱粉類、ステアリン酸等の脂肪酸、ステアリン酸カルシウム・ステアリン酸マグネシウム等の脂肪酸塩、タルク、植物油、ステアリンアルコール・ベンジルアルコール等のアルコール、ガム、ポリアルキレングリコール等が挙げられる。これらのうち液状担体の例としては、一般に水、生理食塩水、デキストロースまたは類似の糖溶液、エチレングリコール、プロピレングリコール、ポリエチレングリコール等のグリコール類が挙げられる。

## 【 0 0 8 5 】

本発明は、NF- $\kappa$ Bの活性化阻害剤または活性化剤としての活性について化合物をスクリーニングするためのキットである。該キットは、

(a) NF- $\kappa$ Bを活性化する作用を有するタンパク質をコードする遺伝子およびNF- $\kappa$ Bの活性化後、その活性化が検出可能なシグナルを提供する成分を含有する細胞、

(b) 該検出可能なシグナルを測定するための試薬、から成り、NF- $\kappa$ Bの活性化を阻害または促進する化合物をスクリーニングするために必要な試薬類を含む。

## 【 0 0 8 6 】

別の側面において、本発明は、

(a) 配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177で表されるヌクレオチド配列を有する本発明のポリヌクレオチド；

(b) (a) のヌクレオチド配列に相補的なヌクレオチド配列；

(c) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176または178で表されるアミノ酸配列を有する本発明のタンパク質またはそれらの断片；または

(d) (c) の本発明のタンパク質に対する抗体；  
を含む診断キットに関する。

#### 【 0 0 8 7 】

少なくとも (a) ～ (d) のいずれかを含むキットは、炎症、自己免疫疾患、感染性疾患（たとえば HIV 感染）および癌などの疾患または該疾患への感受性を診断するのに有用である。

#### 【 0 0 8 8 】

NF- $\kappa$ B は、炎症、自己免疫疾患、ガン及びウイルス感染などの多種の病理



学的状態におけるその関与のため、薬物デザイン及び治療介入のための魅力的な標的である。多数の実験が、NF- $\kappa$ B活性の阻害が深い生理学的作用を有し得ることを示している（たとえば、Ann. Rheum. Dis. 57, 738-741 (1998), American Journal of Pathology 152, 793-803 (1998), ARTHRITIS & RHEUMATISM 40, 226-236 (1997), Am. J. Respir. Crit. Care Med. 158, 1585-1592 (1998), J. Exp. Med. 188 1739-1750 (1998), Gut 42, 477-484 (1998), The Journal of Immunology 161, 4572-4582 (1998), Nature Medicine 3, 894-899 (1997)）。本明細書中に報告するNF- $\kappa$ Bを活性化する作用を有する新規タンパク質の発見により、異常なNF- $\kappa$ B機能を阻害する新しい方法が提供された。さらなる具体例において、本発明は、NF- $\kappa$ Bの活性化を阻害するための前記のNF- $\kappa$ Bを活性化する作用を有するタンパク質の機能を阻害する化合物を用いる方法に関する。上記スクリーニング方法によって得られた、NF- $\kappa$ Bの活性化を阻害する化合物は、たとえば炎症、自己免疫疾患、感染症（1例としてHIV感染症）、ガンなどの、NF- $\kappa$ Bの望ましくない活性化によって特徴つけられる疾患の治療または予防する医薬として有用である。更に、NF- $\kappa$ Bの活性化が細胞のアポトーシスを阻害することが、最近明らかになりつつある。上記スクリーニング方法によって得られた、NF- $\kappa$ Bの活性化を阻害する化合物は、アポトーシスを促進する機能を持つ可能性も考えられる。アポトーシスの誘導が治療につながる疾患としては、腫瘍が挙げられる。

## 【 0 0 8 9 】

逆に、アポトーシスの抑制が治療につながる疾患としてはGVHD、Toxic epidermal necrolysis (TEN)などの皮膚疾患、増殖性腎炎（IgA腎炎、紫斑病性腎炎、ループス腎炎）、劇症肝炎などが挙げられる。よって、上記スクリーニング方法によって得られた、NF- $\kappa$ Bの活性化を促進する化合物はこれらの疾患の治療または予防のための医薬として有用である。

## 【 0 0 9 0 】

更に、本発明のタンパク質をコードする遺伝子は、癌、自己免疫疾患、アレルギー性疾患、および炎症性応答を初めとする様々な疾患の治療を目的とした遺伝



子治療にも有用である。遺伝子治療とは、疾病の治療を目的として、遺伝子または遺伝子を導入した細胞をヒトの体内に投与することを意味する。本発明のタンパク質や該タンパク質をコードするDNAは、診断目的にも使用できる。

## 【 0 0 9 1 】

本発明のスクリーニング方法を用いて得られる化合物またはその塩を上述の医薬組成物として使用する場合、常套手段に従って実施することができる。たとえば、錠剤、カプセル剤、エリキシル剤、マイクロカプセル剤、無菌性溶液、懸濁液剤などとすることができる。このようにして得られる製剤は安全で低毒性であるので、たとえば、ヒトや哺乳動物（たとえば、ラット、ウサギ、ヒツジ、ブタ、ウシ、ネコ、イヌ、サルなど）に対して投与することができる。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射など当業者に公知の方法により行いうる。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。また、該化合物がDNAによりコードされうるものであれば、該DNAを遺伝子治療用ベクターに組み込み、遺伝子治療を行うことも考えられる。投与量、投与方法は、患者の体重や年齢、症状などにより変動するが、当業者であれば適宜選択することが可能である。すなわち本発明は、上記化合物を有効成分として含有する医薬に関する。

## 【 0 0 9 2 】

さらに、上記化合物は、炎症、自己免疫疾患、ウイルス性疾患、感染症、ガンなどの、NF- $\kappa$ Bの望ましくない活性化によって特徴つけられる疾患の治療または予防する医薬として有用である。すなわち本発明は、上記化合物を含む炎症、自己免疫疾患、ウイルス性疾患、ガンなどの医薬に関する。具体的には、例えば、慢性関節リウマチ、変形性関節症、全身性エリテマトーデス、糖尿病、敗血症、喘息、アレルギー性鼻炎、虚血性心疾患、炎症性腸疾患、くも膜下出血、ウイルス肝炎、エイズ、などに対する治療及び予防薬として有用である。

## 【 0 0 9 3 】

さらにまた、本発明は、炎症、自己免疫疾患、ウイルス性疾患、ガンなどの医薬の製造における上記（14）記載の方法により製造された医薬組成物の使用も含む。また本発明は、上記（3）～（6）に記載の遺伝子に対するアンチセンス

オリゴヌクレオチドである。アンチセンスオリゴヌクレオチドは、標的とした遺伝子配列に対して相補的な配列を持つオリゴヌクレオチドを用いて、タンパク質への翻訳、細胞質への輸送、あるいは全体的な生物活性機能に必要な他の活性等のRNAの機能を阻害することによって、標的遺伝子の発現を抑制することができる。この際、アンチセンスオリゴヌクレオチドとしては、RNAを用いても良いし、DNAを用いても良い。本発明のDNA配列は、本発明のタンパク質をコードする遺伝子から転写されたmRNAとハイブリダイズし得るアンチセンスオリゴヌクレオチドを作製するために使用できる。一般にアンチセンスオリゴヌクレオチドが、その遺伝子の発現に対して抑制的に作用することは公知での事実である（たとえば、細胞工学 Vol. 13 No. 4 (1994)）。本発明のタンパク質をコードする遺伝子に対するアンチセンスコード配列を有するオリゴヌクレオチドは、標準の方法で細胞内に導入することができ、該オリゴヌクレオチドは、本発明のタンパク質をコードする遺伝子のmRNAの翻訳を効果的に遮断して、その発現を遮断して、望ましくない作用が阻害される。

## 【 0 0 9 4 】

本発明のオリゴヌクレオチドは、天然に見出されるオリゴヌクレオチドの他に、修飾されたものであっても良い〔たとえば、村上&牧野：細胞工学 Vol. 13 No. 4 p 259-266 (1994)、村上章：蛋白質核酸酵素 Vol. 40 No. 10 p 1364-1370 (1995)、竹内恒成ら：実験医学 Vol. 14 No. 4 p 85-95 (1996)〕。従って、オリゴヌクレオチドは変化した糖部分あるいは糖間部分を有していても良い。これらの例は、当該技術分野において使用が知られているホスホチオエート及び他のイオウ含有種である。幾つかの好ましい態様に従えば、オリゴヌクレオチドの少なくとも一つのホスホジエステル結合が、その活性が調節されるべきRNAが位置する細胞の領域に浸透する組成物の能力を高める機能を有する構造により置換される。

## 【 0 0 9 5 】

このような置換は、ホスホチオエート結合、ホスホロアミデート結合、メチルホスホネート結合または短鎖アルキルもしくはシクロアルキル構造を含むこと

が好ましい。オリゴヌクレオチドはまた、少なくとも幾つかの修飾されたヌクレオチド型を含んでいても良い。従って、天然に通常見いだされるものの以外のプリン及びピリミジンを使用していても良い。同様に本発明の本質的な意図が実行される限り、ヌクレオチドサブユニットのフラノシル部分を修飾することもできる。このような修飾の例は、2'-O-アルキル-、及び2'-ハロゲン置換ヌクレオチドである。本発明において有用な幾つかの糖部分の2'位の修飾の例は、OH、SH、SCH<sub>3</sub>、OCH<sub>3</sub>、OCN、またはO(CH<sub>2</sub>)<sub>n</sub>CH<sub>3</sub>（ここでnは1から約10である）、及び同様の特性を有する他の置換基である。全てのこのような類似体は、本発明の遺伝子のmRNAとハイブリダイズしてそのRNAの機能を阻害する機能を果たす限り、本発明に包含される。

## 【0096】

本発明のオリゴヌクレオチドは、約3から約50ヌクレオチドを含み、約8から約25ヌクレオチドを含むことが好ましく、約12から約20ヌクレオチドを含むことがさらに好ましい。本発明のオリゴヌクレオチドは、周知の方法である固相合成法により作製することができる。このような合成のための装置は、Applied Biosystemsを含む幾つかの業者により販売されている。ホスホチオエート等の他のオリゴヌクレオチドの製造も当業者に公知の方法で作製できる。

## 【0097】

本発明のオリゴヌクレオチドは、本発明の遺伝子から転写されるmRNAとハイブリダイズできるように設計される。与えられた遺伝子の配列に基づいてアンチセンスオリゴヌクレオチドを設計する方法は、当業者であれば容易である〔たとえば、村上および牧野：細胞工学 Vol. 13 No. 4 p 259-266 (1994)、村上章：蛋白質核酸酵素 Vol. 40 No. 10 p 1364-1370 (1995)、竹内恒成ら：実験医学 Vol. 14 No. 4 p 85-95 (1996)〕。最近の研究は、mRNAの5'領域、好ましくは翻訳開始部位を含む領域に設計されたアンチセンスオリゴヌクレオチドが、遺伝子の発現の阻害に最も効果的であることを示唆している。アンチセンスオリゴヌクレオチドの長さは、15から30ヌクレオチドが好ましく、20から2

5ヌクレオチドがより好ましい。ホモロジー検索で他のmRNAとの相互作用がないこと、オリゴヌクレオチド配列内で二次構造を取らないことを確認しておくことは重要である。設計したアンチセンス分子が機能したかどうかの評価は、適当な細胞を用いて、該細胞にアンチセンスオリゴヌクレオチドを導入し、当業者には公知の方法で、対象mRNAの量（たとえば、ノーザンブロットまたはRT-PCR法）、あるいは対象タンパク質の量（たとえば、ウェスタンブロットまたは蛍光抗体法）を測定することにより、発現抑制の効果を確認できる。

## 【 0 0 9 8 】

一方、三重らせん形成（トリプル・ヘリックス技術）は、核内のDNAを標的とした、主に転写の段階での遺伝子発現制御方法である。オリゴヌクレオチドは、主に転写に関与する遺伝子領域に設計され、それにより、転写及び本発明のタンパク質の産生を抑える。これらのRNA、DNA、オリゴヌクレオチドは、公知の合成装置などを用いて製造することができる。

## 【 0 0 9 9 】

本発明のオリゴヌクレオチドは、標的核酸配列を含む細胞に、たとえばリン酸カルシウム法、リポフェクション法、エレクトロポレーション法、マイクロインジェクション法などのDNAトランスフェクション法、またはウイルスなどの遺伝子導入ベクターの使用を含む遺伝子導入法のいずれを用いて導入してもよい。適切なレトロウイルスベクターを用いてアンチセンスオリゴヌクレオチド発現ベクターを作製し、その後、該発現ベクターを細胞と*in vivo*または*ex vivo*で接触させることにより、標的核酸配列を含む細胞に導入できる。

本発明のDNAは、アンチセンスRNA/DNA技術またはトリプル・ヘリックス技術を用いて、本発明のタンパクを介するNF- $\kappa$ Bの活性化を阻害するのに使用できる。

## 【 0 1 0 0 】

本発明のタンパク質をコードする遺伝子のアンチセンスオリゴヌクレオチドは、たとえば炎症、自己免疫疾患、感染症（たとえば、HIV感染症）、ガンなどの、NF- $\kappa$ Bの望ましくない活性化によって特徴つけられる疾患を治療または予防する医薬として有用である。すなわち、本発明は、上記アンチセンスオリ

ゴヌクレオチドを有効成分として含有する医薬である。また、本発明のアンチセンスオリゴヌクレオチドは、ノーザンハイブリダイゼーション法またはPCR法を用いてそれらの疾病の検出に利用することもできる。

## 【 0 1 0 1 】

本発明は、NF- $\kappa$ Bの活性化を阻害するリボザイムも含む。リボザイムは、核酸のヌクレオチド配列を認識して、核酸を切断する活性を持つRNAである（たとえば、柳川弘志 実験医学バイオサイエンス12、RNAのニューエイジ）。リボザイムは、選択された標的RNA、たとえば本発明のタンパク質をコードするmRNAを開裂するように製造することができる。本発明のタンパク質をコードするDNAのヌクレオチド配列を基に、本発明のタンパク質のmRNAを特異的に切断するリボザイムを設計することができ、かようなリボザイムは本発明のタンパク質のmRNAに対して相補的な配列を有し、該mRNAと相補的結合し、ついで該mRNAが開裂され本発明のタンパク質の発現が減少し（または完全に発現せず）、発現減少のレベルは標的細胞内でのリボザイム発現のレベルに依存している。

## 【 0 1 0 2 】

よく用いられるリボザイムには、ハンマーヘッド型とヘアピン型の2種類があり、特にハンマーヘッド型リボザイムは切断活性に必要な一次構造や二次構造がよく調べられており、当業者であれば、本発明のタンパク質をコードするDNAのヌクレオチド配列情報のみで容易にリボザイムの設計が可能である〔たとえば、飯田ら：細胞工学Vol.16 No.3,p438-445 (1997)、大川&平比良：実験医学Vol.12 No.12 p83-88(1994)〕。ハンマーヘッドリボザイムは、標的RNAと相補鎖を形成する2ヶ所の認識部位（認識部位Iと認識部位II）と活性部位からなる構造をなし、標的RNAと認識部位で相補対を形成した後、標的RNAのNUXの配列（N：AまたはGまたはCまたはU、X：AまたはCまたはU）の3'末端側で切断することが知られており、特にGUC（あるいはGUA）が一番高い活性を持つことが知られている〔たとえばKoizumi,Mら：Nucl. Acids Res.17,7059-7071(1989)、飯田ら：細胞工学Vol.16No.3,p438-445 (1997)、大川&平比良：実験医学Vol.12 No.12 p83-88(1994)、川崎&多比良：実験医学 Vol.18 No.3 p3



81-386 (2000)]。

【 0 1 0 3 】

そこでまず、本発明のDNA配列の中からGTC（またはGTA）の配列を探し出し、その前後で数ヌクレオチドから十数ヌクレオチドの相補対をつくることができるようにリボザイムを設計する。設計したリボザイムの適切性の評価は、たとえば、大川&平比良の文献〔実験医学Vol.12 No.12 p83-88(1994)〕に記載の方法によって、作製したリボザイムが、インビトロで標的mRNAを切断できるかどうかを調べることで評価できる。リボザイムの調製は、RNA分子を合成するための当分野で周知の方法により調製する。

【 0 1 0 4 】

別法としては、リボザイムの配列をDNA合成機で合成し、たとえばT7或いはSP6のような適切なRNAポリメラーゼプロモータを有する多種のベクターに組み込み、インビトロで酵素的にRNAを合成させる方法が挙げられる。これらのリボザイムは、たとえばマイクロインジェクション法などの遺伝子導入方法によって細胞内に導入できる。あるいは別の方法として、リボザイムDNAを適当な発現ベクターに組み込んで、株細胞、細胞或いは組織内に導入する。選択された細胞中にリボザイムを導入するのに、適切なベクターを使用することができ、たとえばプラスミドベクター、動物ウイルス（たとえばレトロウイルス、アデノウイルス、ヘルペスあるいはワクシニアウイルス）ベクターがこれらの目的に通常用いられるこれらのリボザイムは、本発明のタンパク質で仲介されるNF- $\kappa$ Bの活性化を阻害する作用を有する。

【 0 1 0 5 】

本発明はまた、機能を有する新規遺伝子の取得方法であり、オリゴキャッピング法を用いて完全長cDNAライブラリーを作製する方法および該機能を有するタンパク質の存在を示すシグナル因子を用いる方法からなる取得方法に関する。シグナル因子には、たとえばレポーター遺伝子が挙げられる。

【 0 1 0 6 】

機能を有する遺伝子（cDNA）を多数取得するためには、不完全長のものが多いcDNAライブラリーを用いると効率が悪い。したがって、全体のクローン



の中で、完全長のものの割合が高いライブラリーが必要となる。完全長 cDNA は遺伝子から出来る mRNA の完全なコピーのことである。オリゴキャッピング法で作製した cDNA ライブラリーは、完全長 cDNA の割合が 50 ～ 80 % であり、従来の方法で作製された cDNA ライブラリーと比べて、5 ～ 10 倍の完全長 cDNA クローンの濃縮になっている（菅野純夫：月刊 BIO INDUSTRY Vol .16 No.11 p19-26）。完全長 cDNA は、遺伝子の機能解析においては、タンパク質発現のために必須なクローンであり、完全長 cDNA のクローンそのものが活性測定のための材料として極めて重要なものであるため、遺伝子の機能解析を試みるに際して、完全長 cDNA のクローニングは必須の要件である。さらにその配列を決定することで、それがコードするタンパク質の一次配列を確定するための重要な情報となると同時に、遺伝子の全エクソンの配列も分かる。すなわち、完全長 cDNA は、遺伝子を同定する上で貴重な情報、たとえばタンパク質の一次配列、エクソン-イントロン構造、mRNA の転写開始点、プロモーターの位置などを決めるための情報をも与える。

## 【 0 1 0 7 】

オリゴキャッピング法による完全長 cDNA ライブラリー作製は、たとえば実験医学別冊新遺伝子工学ハンドブック改訂第 3 版（1999 年）に記載の方法に従い行うことができる。機能を有するタンパク質の存在を示すレポーター遺伝子は、転写因子等のタンパク質因子が結合できる適切な発現制御配列部分（1 つまたは複数）と、その転写因子等による活性化を測定できる構造遺伝子部分からなる。構造遺伝子部分は、その発現産物の活性または生産量（mRNA の生産量も含まれる）を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコールアセチルトランスフェラーゼ、 $\beta$ -ガラクトシダーゼ、ルシフェラーゼ等を用いることができ、その酵素活性を測定することで利用できる。

## 【 0 1 0 8 】

本発明において、オリゴキャッピング法とは、鈴木・菅野 実験医学別冊 遺伝子工学ハンドブック改訂第 3 版に記載のように、BAP, TAP, RNA リガーゼにより、キャップ構造を合成オリゴに置換する方法である。

## 【 0 1 0 9 】

本発明の方法は、イン ビトロ (in vitro) の系、あるいは細胞を用いて (cell-based) の系のどちらの方法でも良く、好ましくは細胞を用いた系である。細胞は、原核大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良く、好ましくは動物細胞であり、293EBNA細胞、NIH3T3細胞が例示できる。

## 【 0 1 1 0 】

機能を有するタンパク質の存在を示すレポーター遺伝子としては、本願明細書に示したNF- $\kappa$ Bのレポーター遺伝子の他に、たとえばCREB (cAMP responsive element binding protein) 結合配列あるいはAP-1 (activator protein-1) 結合配列をレポーター遺伝子の発現制御配列部分に有するレポーター遺伝子が挙げられる。たとえば、CREBを活性化する機能を有する遺伝子を取得したい場合は、CREB依存レポータープラスミドとオリゴキャッピング法で作製した完全長cDNAクローンを細胞に共導入し、その中からレポーター活性が上昇したプラスミドを選ぶことによって、該目的を達成することができる。また、CREBを抑制する機能を有する遺伝子を取得したい場合は、CREB依存レポータープラスミドとオリゴキャッピング法で作製した完全長cDNAクローンを細胞に共導入し、その中からレポーター活性が減少したプラスミドを選ぶことによって、該目的を達成することができる。この場合、細胞に何らかの刺激を加えた状態で行なっても良い。cDNAクローンの細胞への導入は、1クローンでも良いし、複数のクローンを同時に導入しても良い。本発明の該方法の一例は、本願明細書実施例に詳細に記述してある。あるいは、完全長cDNAとレポーター遺伝子を細胞に導入した後、細胞をIL-1あるいはTNF- $\alpha$ などで刺激し、レポーター活性の上昇の弱いクローンを選ぶことによって、NF- $\kappa$ Bの活性化を抑制する機能を有する遺伝子を取得するためのスクリーニング系を構築することもできる。

## 【 0 1 1 1 】

しかしながら、本発明の該方法は、この方法に限定されるものではない。また、本発明のcDNAは、完全長cDNAであるため、その5'末端の配列がmR

NAの転写開始点であり、該cDNA配列をゲノムのヌクレオチド配列と比較することにより、該遺伝子のプロモーター領域を同定することに利用できる。ゲノムのヌクレオチド配列は、データベースに公知の配列として登録されている場合はその配列を利用できる。あるいは、該cDNAを用いてたとえばハイブリダイゼーションによってゲノムライブラリーからクローニングし、ヌクレオチド配列を決めることもできる。このようにして、本発明のcDNAのヌクレオチド配列をゲノムの配列と比較することによって、その上流に存在する該遺伝子のプロモーター領域を同定することが可能である。さらに、このようにして同定した該遺伝子のプロモーター断片を用いて該遺伝子の発現を調べるレポータープラスミドを作製することができる。レポータープラスミドは、大方の場合、転写開始点からその上流2 kb、好ましくは転写開始点からその上流1 kbのDNA断片をレポーター遺伝子の上流に組み込むことによって作製できる。さらに該レポータープラスミドは、該遺伝子の発現を増強あるいは減弱させる化合物のスクリーニングに利用できる。具体的には例えば、該レポータープラスミドで適当な細胞を形質転換し、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することによりスクリーニングすることができる。これらも本発明に含まれる。

#### 【 0 1 1 2 】

また本発明は、配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177で表されるヌクレオチド配列のうち少なくとも1以上を含むデータセットおよび／または配列番号

1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176および178で表されるアミノ酸配列のうち少なくとも1以上を含むデータセットを保存したコンピュータ読み込み可能媒体に関する。

## 【0113】

さらに本発明は、上記に記載の媒体上のデータと他のヌクレオチド配列のデータを比較して相同性の算出を行う方法に関する。すなわち、本発明の遺伝子およびアミノ酸配列は、その2次元および3次元構造を決定し、たとえば同様の機能を有する相同性の高いさらなる配列を同定するための貴重な情報源となる。これらの配列をコンピュータ読み込み可能媒体に保存し、ついで既知の高分子構造プログラムにおいて保存したデータを用いて、GCGのような既知検索ツールを用いてデータベースを検索すれば、データベース中の、ある相同性を有する配列を見出すことは容易である。

## 【0114】

コンピュータ読み取り可能媒体は情報またはデータを保存するのに用いる物体のいずれの組成物であってもよく、たとえば、市販フロッピーディスク、テープ、チップ、ハードドライブ、コンパクトディスク、およびビデオディスク等がある。また、本媒体上のデータは、他のヌクレオチド配列のデータと比較して相同性の算出を行なう方法を可能にする。この方法には、本発明ポリヌクレオチド配列を含む第一のポリヌクレオチド配列をコンピュータ読み込み可能媒体中に提供し、次いで、該第一のポリヌクレオチド配列を少なくとも一つの第二のポリヌクレオチドまたはポリペプチド配列と比較して相同性を同定する工程を含む。

## 【0115】

本発明はまた、配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175 または 177 から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質に関する。DNA プローブである複数の各種ポリヌクレオチドがスライドガラス等の特別に加工された基質上に固定され、次いで標識された標的ポリヌクレオチドを、固定化されたポリヌクレオチドとハイブリダイズさせ、それぞれのプローブからのシグナルを検出する。得られるデータは、解析され、遺伝子発現が測定される。

## 【 0 1 1 6 】

本発明はさらにまた、配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176 または 178 で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質に関する。このタンパク質を固定した不溶性基質と、生物由来の細胞抽出液とを混合し、不溶性基質上に捕獲された、診断あるいは新薬開発のために有効であることが期待されるタンパク質などの細胞由来の成分を、



単離あるいは同定することができる。

【0117】

【実施例】

以下に、実施例を挙げて本発明を詳しく説明するが、本発明は、これらの例に何ら限定されるものではない。

【0118】

(実施例1) オリゴキャッピング法を用いた完全長cDNAライブラリーの作製

(1) ヒト肺線維芽細胞 (Cryo NHLF) からのRNA調製

ヒト肺線維芽細胞 (Cryo NHLF: 三光純薬株式会社より購入) を、添付のプロトコールに従って培養した。10cmシャーレ50枚まで継代培養した後、セルスクレーパーで細胞を回収した。次いで、回収した細胞からRNA抽出用試薬ISOGEN (ニッポンジーンより購入) を用いて全RNAを取得した。取得の具体的方法は、試薬のプロトコールに従った。次いで、オリゴ-dT セルロース カラムを用いて、全RNAからポリA+RNAを取得した。ポリA+RNA取得の具体的方法は、上記Maniatisの実験書に従った。

【0119】

(2) マウスATDC5細胞からのRNA調製

マウスEC (embryonal carcinoma) 由来クローン化細胞株ATDC5 (Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116 (1990)) を10cmシャーレ50枚まで継代培養した後、上記(1)と同様の方法でポリA+RNAを取得した。

【0120】

(3) オリゴキャッピング法による完全長cDNAライブラリー作製

上記ヒト肺線維芽細胞とATDC5細胞のポリA+RNAから、オリゴキャッピング法により完全長cDNAライブラリーをそれぞれ作製した。オリゴキャッピング法による完全長cDNAライブラリー作製の具体的方法は、菅野らの方法 [たとえば、Maruyama, K. & Sugano, S. Gene, 138: 171-174 (1994)、Suzuki, Y. et al. Gene, 2



00:149-156 (1997)、鈴木・菅野 実験医学別冊 遺伝子工学ハンドブック改訂第3版]に従って作製した。

【0121】

(4) プラスミドDNAの調製

上記実施例で作製した完全長cDNAライブラリーを、エレクトロポレーション法によって大腸菌TOP10株に形質転換した後、 $100\mu\text{g}/\text{ml}$ アンピシリンを含有するLB寒天培地に塗布し、 $37^\circ\text{C}$ で一晩インキュベートした。続いて、アンピシリン含有LB寒天培地上で生育した大腸菌のコロニーから、QIAGEN社のQIAwell 96 Ultra Plasmid Kitを用いてプラスミドを回収した。具体的方法は、QIAwell 96 Ultra Plasmid Kitに添付のプロトコールに従った。

【0122】

(実施例2) NF- $\kappa$ Bを活性化する作用を有するDNAのクローニング

(1) NF- $\kappa$ Bを活性化する作用を有するタンパク質をコードするcDNAのスクリーニング

293-EBNA細胞 (Invitrogen社より購入) を細胞培養用96穴プレートに $1 \times 10^4$  Cells/wellとなるように、5% FBS存在下のDMEM培地を用い、24時間 $37^\circ\text{C}$ で培養した(5%  $\text{CO}_2$ 存在下)。次いで、FuGENE 6 (Roche社より購入) を用いて、pNF $\kappa$ B-Luc (STRATAGENE社より購入) 50 ngと、上記実施例1. (4) で調製した完全長cDNA  $2\mu\text{l}$  を1ウェルに共導入した。導入の方法は添付のプロトコールに従った。24時間 $37^\circ\text{C}$ で培養後、ロングタームルシフェラーゼアッセイシステム、ピッカジーンLT2.0 (東洋インキ社) を用いて添付されている説明書に従い、NF- $\kappa$ Bのレポーター活性 (ルシフェラーゼ活性) を測定した。なおルシフェラーゼ活性は、Perkin Elmer社のWallac ARVOTMST 1420 MULTILABEL COUNTERを用いて行った。

【0123】

(2) ヌクレオチド配列の決定

上記スクリーニングを155000クローン行い、ルシフェラーゼ活性が対照実験（完全長cDNAの代わりに、空ベクターpME18S-FL3を導入した細胞のルシフェラーゼ活性）と比べて5倍以上上昇しているプラスミドを選抜し、まず、クローニングされているcDNAの5'側（シーケンスプライマー：5'-CTTCTGCTCTAAAAGCTGCG-3'（配列番号179）と3'側（シーケンスプライマー：5'-CGACCTGCAGCTCGAGCACAA-3'（配列番号180））からそれぞれone-passシーケンスを行ない、できる限り長く決定した。なお、ヌクレオチド配列決定のための試薬や方法は、Thermo Sequenase II Dye Terminator Cycle Sequencing Kit（アマシャム ファルマシア社）、あるいはBigDye Terminator Cycle Sequencing FS Ready Reaction Kit（アプライドバイオシステムズ社）を用い、ABI PRISM 377シーケンサー、あるいは、ABI PRISM 3100シーケンサーを用い、各々キットに添付されている説明書に従って行なった。

## 【0124】

## （3）得られたクローンのデータベース解析

得られたヌクレオチド配列について、GenBankに対するBLAST（Basic local alignment search tool）[S. F. Altschul et al., J. Mol. Biol., 215: 403-410 (1990)] 検索を行なった。その結果、147クローンがNF-κBを活性化する作用を有する新規のタンパク質をコードする89種類の遺伝子であった。

## 【0125】

## （4）全長シーケンス

89種類の新規のクローンについて全長ヌクレオチド配列（配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、1

02、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175または177)を決定し、タンパク質をコードする部分(オープンリーディングフレーム)のアミノ酸配列(配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176および178)を予想した。

#### 【0126】

(実施例3) NF- $\kappa$ Bの活性化を阻害する化合物のスクリーニング

293-EBNA細胞を細胞培養用96wellプレートに、 $1 \times 10^4$  Cells / 100  $\mu$ l / wellの細胞数になるように、5% FBS存在下のDMEM培地にまき、5% CO<sub>2</sub>存在下、37°Cで24時間培養した。次いで、FUGENE 6を用いて、上記実施例2で得た、配列番号41のNF- $\kappa$ Bを活性化作用を有するタンパク質をコードする遺伝子を含むプラスミド10ngと、レポータープラスミドpNF $\kappa$ B-Luc50ngを1wellに共導入した。1時間後、プロテアソーム阻害剤であることが知られているMG132 (CALBIOCHEMより購入) (Uehara T. et. al. J. Biol. Chem. 274 p15875-15882 (1999)、Wang X C. et al. Invest. Ophthalmol. Vis. Sci. 40 p477-486)を終濃度10  $\mu$ Mになるように培養液中に加えた。37°Cで24時間培養後、ピッカジーンLT2.0を用いてレポーター活性を測定した

。その結果、MG 1 3 2 はレポーター遺伝子の発現を抑制した（図 1）。

【 0 1 2 7 】

【発明の効果】

本発明により、産業上有用性の高い NF- $\kappa$ B を活性化する作用を有するタンパク質やそれらの遺伝子が提供された。本発明のタンパク質やそれらの遺伝子により、NF- $\kappa$ B の過剰な活性化、又は阻害が関与する疾患の治療や予防に有用な化合物のスクリーニング、さらにそのような疾患の診断薬を作製することが可能である。更に本発明の遺伝子は、遺伝子治療に用いられる遺伝子ソースとしても有用である。

【 1 2 8 】

【配列表】

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190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser

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Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr

210

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220

Pro Ser Gly Met Val Phe His Arg Val

225

230

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<211> 2409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(923)

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

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50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

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aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

115

gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc 620

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val

120

125

130

tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg 668

Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp

135

140

145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc 716

Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe

150

155

160

aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat 764

Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp

165

170

175

180

gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag 812

Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu

185

190

195

gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat 860

Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His .

200

205

210

ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg 908

Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met

215

220

225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag 963

Val Phe His Arg Val

230

ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg 1023

gatcagcacg agcggaaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt 1083

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tttttt 2409

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<211> 198

<212> PRT

<213> Homo sapiens

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Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp

20 25 30

Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro

35 40 45

Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys  
50 55 60

Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro  
65 70 75 80

Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg  
85 90 95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu  
100 105 110

Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile  
115 120 125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp  
130 135 140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala  
145 150 155 160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln  
165 170 175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp  
180 185 190

Arg His Val Val Leu Ser

195

<210> 10

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

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<222> (86)..(679)

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Met Ala Thr Leu Trp Gly Gly Leu Leu

1

5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160

Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu

10

15

20

25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208

Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg

30

35

40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256

Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

45

50

55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304

Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

60

65

70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352

Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

75

80

85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400

Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile

90

95

100

105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448

Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr

110

115

120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496

Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala

125

130

135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544

Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala

140

145

150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592

Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu

155

160

165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640  
 Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu  
 170 175 180 185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689  
 Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser  
 190 195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggtttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaaact 809

ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttta 869

aagcacacag ctcaaagtca gccataaagt cttttcctat ttgtgacttt tactaataaa 929

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ttgcaataaa gaaattttat ttttaaacc 1498

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<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

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Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

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30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35

40

45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50

55

60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65

70

75

80



Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu  
85 90 95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile  
100 105 110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe  
115 120 125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala  
130 135 140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp  
145 150 155 160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly  
165 170 175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe  
180 185 190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr  
195 200 205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr  
210 215 220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

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<222> (153)..(815)

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gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173

Met Ala Leu Ala Leu Ala Ala

1

5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221

Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269

Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25

30

35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317

Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

40

45

50

55

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365

Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

60

65

70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413

Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75

80

85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461

Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90

95

100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509

Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met

105

110

115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557

Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu

120

125

130

135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605

Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser

140

145

150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653

Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser

155

160

165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701

Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val

170

175

180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749

Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr

185

190

195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797

Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr

200

205

210

215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845

Arg Val Leu Phe Ile Tyr

220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca 905

gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965

tctctatttg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

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<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

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Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

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25

30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu

35

40

45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50

55

60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65

70

75

80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85

90

95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100

105

110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115

120

125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe

130

135

140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145

150

155

160



Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu  
 165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr  
 180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu  
 195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg  
 210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe  
 225 230 235 240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 14

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1

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ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65

70

75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339

Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387

Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe  
110 115 120 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435  
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu  
130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483  
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser  
145 150 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531  
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly  
160 165 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579  
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp  
175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627  
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe  
190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675  
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu  
210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723  
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225

230

235

tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccatth ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatatth gcatatactt gatagaaacc ataaagttgt agcagtttaag 1018

tccagtcaca ttgtggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

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taacctgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatthta aattaagtga actaaatata tatgtgtata tgtatacaca tatatatata 1438

cacacacata tatatatthta gaaacgtgag tgttaaagat agaatttgth ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

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aagagatcct gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

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gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatcct gcaaatcatt ttatgtctca 2038

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<213> Homo sapiens

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35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val  
50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro  
65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu  
85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln  
100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

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Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe		
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Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile		
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		160
Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu		
	165	170
		175
Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr		
180	185	190
Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu		
195	200	205
Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg		
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Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe		
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<212> DNA

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

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Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

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20

25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

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35

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45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

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55

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Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

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Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

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85

90

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Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu

95

100

105

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Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

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115

120

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agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435

Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

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140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483

Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

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ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531

Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly

160

165

170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175

180

185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627

Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190

195

200

205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675

Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723

Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

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tat ttc ttc tta ttg tagagactgc atcaaccgga cattcctttc ttataccaat 778

Tyr Phe Phe Leu Leu

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caagccattt ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata 958

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tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

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<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

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30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35

40

45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50

55

60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65

70

75

80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

85

90

95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu

100

105

110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro

115

120

125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr

130

135

140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr

145

150

155

160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro

165

170

175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala

180

185

190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile

195

200

205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln

210

215

220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala





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Met Ala

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

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agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

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gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

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ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

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acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

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105

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tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442

Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115

120

125

130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490

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140

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Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser

150

155

160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586

Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165

170

175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala

180

185

190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682

Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

195

200

205

210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730  
 Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg  
 215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778  
 Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile  
 230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826  
 Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile  
 245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874  
 Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys  
 260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922  
 Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn  
 275 280 285 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970  
 Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu  
 295 300 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018  
 Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu  
 310 315 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

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<213> Homo sapiens

<400> 19

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Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35

40

45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

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55

60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65

70

75

80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

85

90

95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu

100

105

110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro

115

120

125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr  
130 135 140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr  
145 150 155 160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro  
165 170 175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala  
180 185 190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile  
195 200 205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln  
210 215 220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala  
225 230 235 240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn  
245 250 255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu  
260 265 270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr



275

280

285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu

290

295

300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met

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Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

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<213> Homo sapiens

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

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agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

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gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

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ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

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acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

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tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

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95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

100

105

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tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442

Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115

120

125

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cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490  
Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser  
135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538  
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser  
150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586  
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser  
165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634  
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala  
180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682  
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu  
195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730  
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg  
215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778  
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile  
230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826

Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile.

245

250

255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874

Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260

265

270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922

Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275

280

285

290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970

Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018

Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

tagagactgc atcaaccga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

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cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaagcc 1420

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actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatatatta 1780

gaaacgtgag tgttaaagat agaatttggt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaagtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900

ttttcagatg ggaagctgca tttttaggat tgcccatctt aagagatctt gcaggaagag 1960

attgtattag atattatatt tatttcattt aagataattt tcaaagttaa ttttctaat 2020

aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

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<211> 76

<212> PRT

<213> Homo sapiens

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Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val

20

25

30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

35

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Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr

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Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

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<213> Homo sapiens

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cggcctccgc ggtgcctgcc ttcgctctca ggttgaggag ctcaagcttg ggaaa atg 178

Met



gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226  
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys  
5 10 15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274  
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser  
20 25 30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322  
Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys  
35 40 45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370  
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys  
50 55 60 65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423  
Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp  
70 75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaate 543

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aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatcttttg 723

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tt 1085

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<212> PRT

<213> Homo sapiens

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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val

20

25

30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35

40

45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp

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60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser

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Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20

25

30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35

40

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att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

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55

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tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65

70

75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356

Ser Leu Ser Gly Leu

80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggcttttagac 416

attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt 476

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<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu

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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val

20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala

50 55 60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys

65 70 75 80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln

85 90 95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met

100

105

110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly

115

120

125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile

130

135

140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr

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160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala

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170

175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

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<222> (114)..(650)



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Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164

Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

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15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212

Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu

20

25

30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260

Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro

35

40

45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308

Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val

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55

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65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356

Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr

70

75

80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404

Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu

85

90

95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452

Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val

100

105

110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500

His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu

115

120

125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548

Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly

130

135

140

145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596

Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe

150

155

160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644

Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu

165

170

175

ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg 700

Leu Phe

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<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

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Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

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30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35

40

45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50

55

60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe

65

70

75

80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val

85

90

95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp

100

105

110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

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155

160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210

215

220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

225

230

235

240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

245

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255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly

260

265

270

Ile Ala Lys Val Lys Ala Asn

275

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(955)

<400> 28

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tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1

5

10

15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20

25

30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35

40

45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50

55

60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc 358

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe

65

70

75

80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val

85

90

95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp

100

105

110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145 150 155 160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165 170 175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180 185 190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195 200 205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210 215 220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

225 230 235 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc 886

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

245 250 255



aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934  
 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly  
 260 265 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgccacc 985  
 Ile Ala Lys Val Lys Ala Asn  
 275

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ggaaacc 1472

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1

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Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20

25

30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50

55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

75

80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85

90

95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

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110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala

115

120

125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

130

135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145)..(555)

<400> 30

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ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe

10

15

20

25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267

Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro

30

35

40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315  
Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro  
45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363  
Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly  
60 65 70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411  
Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro  
75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459  
Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala  
90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507  
Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser  
110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555  
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu  
125 130 135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtgtg 615

gtgcaggcgc ggttccttac gcccattgtg tgctgtgtgt gtccaggcac ggttccttac 675

gcccattgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735

tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

attatgcttc ctaaaatctc aagccaaact caaagaatgg ggtgggtgggg ggcaccctgt 855

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accctagggt gaccaagtag ggcctgtcac accagggtgg cgcagctttc tgtgtgatgc 975

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gagttggggg taccggttgc agagccaggg acatgatgca ggcgaagctt gggatctggc 1095

caagttggac ttgatcctt tgggcagatg tcccattgct ccctggagcc tgtcatgcct 1155

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catgcacaca cagcctagct gccccaggg agctctgctg cccttgctgg ccctgccctt 1335

cccacaggtg agcagggctc ctgtccacca gcacactcag ttctcttccc tgcagtgttt 1395

tcattttatt ttagccaaac attttgcctg ttttctgttt caaacatkat agttgatatg 1455

agactgaaac ccctgggttg tggagggaaa ttggctcaga gatggacaac ctggcaactg 1515

tgagtccttg cttcccagaca ccagcctcat ggaatatgca acaactcctg taccaccagtc 1575

cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtggggt 1635

gtggggccct ggatggcagc tctggcccag acatgaatac ctcgtgttcc tcctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggtct 1755

gtacacttgt ttataataaa tgcaatcggt tgg 1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85

90

95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Glu Cys Pro Cys Gln Leu

115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(444)

<400> 32

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Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162

Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210

Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258

Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln

60

65

70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354

Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr

75

80

85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402

Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro

90

95

100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444

Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu

105

110

115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggcctctgc ccctttctgc ttgcctgcc ctcacacggc agcccaccat 564



gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

cctggcctct ctggctgcca cttggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744

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cccctgggtt gtggaggga attggctcag agatggacaa cctggcaact gtgagtcctt 1644

gcttcccgac accagcctca tggaatatgc aacaactcct gtaccccagt ccacggtgtt 1704

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tggatggcag ctctggccca gacatgaata cctcgtgttc ctctccctc tattactgtt 1824

tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884

tttataataa atgcaatcgt ttgg 1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln

1

5

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15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala

20

25

30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro

35

40

45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala

50

55

60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val

65

70

75

80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro

85

90

95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala

100

105

110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro

115

120

125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly

130

135

140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly

145

150

155

160

Ser Asp Gly Gly Tyr Thr Ile Trp

165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(573)

<400> 34

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gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1

5

10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159

Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro

15

20

25

30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207

Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr

35

40

45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255

Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser

50

55

60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303  
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val  
65 70 75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351  
Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val  
80 85 90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399  
Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr  
95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447  
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro  
115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495  
Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met  
130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543  
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met  
145 150 155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593  
Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp  
160 165

tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat 653

attaacctga agttgcagtt tagacacatg ttgttggggt gtctttctgg tgcccaaact 713

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atthtgaggt aggggaggta tccattcata aatgaatgt gggatgaagcc gccctaagga 833

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aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta 953

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cgcattagtt gtctgccttt tcttttccat cccttgcccc acccatccca tctccaaccc 1073

tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133

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tcgtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct 1313

gcatacacga acctaaccca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373

aaagatgtcg tgcaaactgt actgtgaaca acagttggtt taaaatatga ggggcaagga 1433

ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493

gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggctcc 1553

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tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaaattgga ttttatittta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcggt 1793

gtatgtctct ctctacactg tggatgcactt aacttggtga atttttatac taaaaatgta 1853

gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu

1

5

10

15

Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp

20

25

30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe

35

40

45

Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly  
50 55 60

Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys  
65 70 75 80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr  
85 90 95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe  
100 105 110

Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly  
115 120 125

Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu  
130 135 140

Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu  
145 150 155 160

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr  
165 170 175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg  
180 185 190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala



195

200

205

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro

210

215

220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly

225

230

235

240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu

245

250

255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys

260

265

270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe

275

280

285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala

290

295

300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr

305

310

315

320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val

325

330

335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile

340

345

350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr  
 355 360 365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala  
 370 375 380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met  
 385 390 395 400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu  
 405 410 415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val  
 420 425 430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala  
 435 440 445

Pro Glu Lys Gln Met Ala Pro  
 450 455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118

Met

1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166

Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5

10

15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214

Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr

20

25

30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262

Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala

35

40

45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310

Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val

50

55

60

65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358

Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val

70

75

80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406  
 Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe  
 85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454  
 Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser  
 100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502  
 Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp  
 115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550  
 Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln  
 130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598  
 Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu  
 150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646  
 Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe  
 165 170 175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg 694  
 Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu  
 180 185 190

ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg 742

Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met  
195 200 205

gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca 790  
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser  
210 215 220 225

ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt 838  
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser  
230 235 240

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta 886  
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu  
245 250 255

agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag 934  
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu  
260 265 270

aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt 982  
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu  
275 280 285

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030  
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr  
290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078  
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg

310

315

320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126

Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys

325

330

335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174

Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val

340

345

350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222

Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala

355

360

365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270

Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln

370

375

380

385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318

Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser

390

395

400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu

405

410

415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414

Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser

420

425

430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462

Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro

435

440

445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510

Glu Lys Gln Met Ala Pro

450

455

gccagtgggt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaaca acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaaggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaagaggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser  
1 5 10 15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala  
20 25 30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser  
35 40 45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile  
50 55 60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser  
65 70 75 80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met  
85 90 95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala  
100 105 110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp  
115 120 125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu  
130 135 140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu



145	150	155	160
Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val			
	165	170	175
Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp			
	180	185	190
Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe			
	195	200	205
Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr			
	210	215	220
Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu			
225	230	235	240
Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly			
	245	250	255
Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg			
	260	265	270
Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His			
	275	280	285
Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser			
290	295	300	

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp  
305 310 315 320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292)..(1257)

<400> 38

tactgctggc ggctggagcg gagcgcaccg cggcgggtggt gcccagagcg gagcgcagct 60

ccctgccccg cccctcccc tcggcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagcc gagtgaagac atttccacct ggacacctga ccatgtgcct gccctgagca 180

gcgaggccca ccaggcatct ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240

tcggcagttg gcaggctccc tctgcagtgg ggtctgggcc tcggccccac c atg tcg 297

Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345  
 Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser  
           5                          10                          15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393  
 Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala  
           20                          25                          30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441  
 Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala  
           35                          40                          45                          50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489  
 Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser  
                           55                          60                          65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537  
 Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr  
                           70                          75                          80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585  
 Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly  
           85                          90                          95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633  
 Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu  
           100                          105                          110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681

Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser  
115 120 125 130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729  
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser  
135 140 145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777  
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu  
150 155 160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825  
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu  
165 170 175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873  
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu  
180 185 190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921  
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr  
195 200 205 210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969  
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala  
215 220 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017  
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu

230

235

240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065

Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys

245

250

255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113

Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn

260

265

270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161

Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile

275

280

285

290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209

Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala

295

300

305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257

Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln

310

315

320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctggt tttatatata tattttttgt tgctggttta acatctccac 1437

gtccctagca t

1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

1 5 10 15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His

20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu

65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu

85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe

100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly  
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile  
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val  
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala  
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly  
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val  
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr  
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met  
225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser  
245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu  
260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro  
275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys  
290 295 300

Gln Met His Ile Trp Met Ser Ser Thr  
305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1091)

<400> 40

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ctccagccgc ccgcggggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5



atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221  
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro  
10 15 20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269  
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg  
25 30 35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317  
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln  
40 45 50 55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365  
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val  
60 65 70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413  
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg  
75 80 85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461  
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro  
90 95 100

aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac 509  
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn  
105 110 115

att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag 557

Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys  
120 125 130 135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag 605  
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys  
140 145 150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg 653  
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg  
155 160 165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg 701  
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr  
170 175 180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct 749  
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser  
185 190 195

gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca 797  
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser  
200 205 210 215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845  
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp  
220 225 230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893  
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe

235

240

245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941

Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln

250

255

260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989

Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg

265

270

275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037

Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp

280

285

290

295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085

Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser

300

305

310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac 1141

Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcaggtt ccccaaaagg ctgccagcc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttggtggaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggtta tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

1

5

10

15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr

20

25

30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

35

40

45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr

50

55

60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro

65

70

75

80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln

85

90

95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn

100

105

110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro

115

120

125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn

130

135

140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala

145

150

155

160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr

165

170

175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe

180

185

190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe

195

200

205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His

210

215

220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr

225	230	235	240
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met			
	245	250	255
Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser			
	260	265	270
Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val			
	275	280	285
Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg			
	290	295	300
Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe			
305	310	315	320
Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln			
	325	330	335
Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr			
	340	345	350
Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg			
	355	360	365
Ala Lys Glu			
370			

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

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ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114

Met Ser His Glu Lys Ser Phe Leu

1

5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162

Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly

10

15

20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210

Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala

25

30

35

40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258

Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly

45

50

55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306  
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly  
60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354  
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly  
75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402  
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr  
90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450  
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe  
105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498  
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu  
125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546  
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp  
140 145 150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594  
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val  
155 160 165

ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act 642



Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr  
170 175 180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690  
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr  
185 190 195 200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738  
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys  
205 210 215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg 786  
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser  
220 225 230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc 834  
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe  
235 240 245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc 882  
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val  
250 255 260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930  
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr  
265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978  
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe

285

290

295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026

Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr

300

305

310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074

Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr

315

320

325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122

Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr

330

335

340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170

Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu

345

350

355

360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223

Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu

365

370

gtgcccgcctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttcccct ctctcttgct cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctcctgtatg tacactgcag atacttccat ttggacccgc tgtggccaca gcatggcccc 1403

tttagtcctc ccgccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463

tactcattgt tgcattgagcc ctgtctgcca gcccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gcccaagaggt gaggggtgcac gtcttcctc ctgtcccagc 1583

tccccagcct ggcgtagagc acccctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

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tgggatttgc tctctgcc 1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1 5 10 15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu  
50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr  
65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg  
85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met  
100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg  
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln  
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala  
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala  
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val  
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu  
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser  
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr  
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly  
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly  
260 265 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala  
275 280 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr  
290 295 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn  
305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu  
325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly  
340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385

390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

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Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100

105

110

115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442

Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly

120

125

130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490

Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val

135

140

145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538

Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe

150

155

160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586

Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val

165

170

175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634

Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His

180

185

190

195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682

Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr

200

205

210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730

Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu

215

220

225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778

Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826

Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255



gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874  
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu  
260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922  
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu  
280 285 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970  
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn  
295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018  
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val  
310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066  
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser  
325 330 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114  
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys  
340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162  
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met  
360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210

Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

375

380

385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258

Gly Pro Glu Lys Glu Asn

390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

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tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

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<212> PRT

<213> Homo sapiens

<400> 45

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Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20

25

30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu  
35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu  
50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr  
65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg  
85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met  
100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg  
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln  
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala  
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala  
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val  
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu  
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser  
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr  
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly  
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly  
260 265 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala  
275 280 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr  
290 295 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn  
305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu  
325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

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Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Gln Asn

385

390

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Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

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10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442

Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly

120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490  
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val  
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538  
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe  
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586  
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val  
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634  
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His  
 180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682  
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr  
 200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730  
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu  
 215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778  
 Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr  
 230 235 240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826



Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile  
245 250 255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874  
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu  
260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922  
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu  
280 285 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970  
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn  
295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018  
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val  
310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066  
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser  
325 330 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114  
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys  
340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162  
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met

360

365

370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210  
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

375

380

385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258  
Gly Pro Glu Lys Gln Asn

390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

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<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

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Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys  
20 25 30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe  
35 40 45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys  
50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile  
65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu  
85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val  
100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val  
115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val  
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<210> 48

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<400> 48

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Met Ile Ser

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tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166

Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val

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ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214

Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu

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25

30

35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262

Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

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tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310

Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala

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60

65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358

Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro  
70 75 80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406  
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg  
85 90 95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454  
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu  
100 105 110 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502  
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val  
120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553  
Gly Glu Ser Asn Asn Met Val  
135

aaatattgtg ttatttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613

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caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

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cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953

caataaaagg gtacttttct att 2976

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<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

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His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln

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25

30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val

35

40

45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro  
50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met  
65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile  
85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser  
100 105 110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu  
115 120 125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp  
130 135 140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg  
145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His  
165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr  
180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu

195

200

205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro

210

215

220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile

225

230

235

240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser

245

250

255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser

260

265

270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe

275

280

285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His

290

295

300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met

305

310

315

320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser

325

330

335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser

340

345

350

Arg Ser Thr Thr His Leu Ile

355

<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (327)..(1403)

<400> 50

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atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

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Met Ser Lys Glu Thr Ile Ile Lys Cys

1

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Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala  
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Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro  
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gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497  
Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys  
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cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545  
His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile  
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Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys  
75 80 85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641  
Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly  
90 95 100 105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689  
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val  
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gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737  
Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val

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Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro

155

160

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gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881

Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys

170

175

180

185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929

Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu

190

195

200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977

Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln

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atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt 1025

Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys

220

225

230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073

Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile

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240

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tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121

Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp

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Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys

270 275 280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217

Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg

285 290 295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265

Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser

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Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu

315 320 325

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Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu

330 335 340 345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403

Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

350 355

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Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln

35 40 45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu  
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Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu  
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Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val  
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Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys  
100 105 110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln  
115 120 125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser  
130 135 140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu  
145 150 155 160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg  
165 170 175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln  
180 185 190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys  
195 200 205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe  
210 215 220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe  
225 230 235 240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr  
245 250 255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu  
260 265 270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys  
275 280 285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu  
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Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met  
305 310 315 320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser  
325 330 335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu  
340 345 350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe

355

360

365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser

370

375

380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp

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400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro

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Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr

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435

440

445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro

450

455

460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val

465

470

475

480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp

485

490

495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu

500

505

510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu  
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Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu  
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu  
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu  
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Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr  
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Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn  
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val  
610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser  
625 630 635 640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp  
645 650 655

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile  
660 665 670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly  
675 680 685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu  
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Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His  
705 710 715 720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val  
725 730 735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp  
740 745 750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp  
755 760 765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn  
770 775 780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys  
785 790 795 800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro  
805 810 815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu

820

825

830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser

835

840

845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu

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855

860

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His Leu Ile

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 Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser  
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 Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser  
 25 30 35 40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196  
 Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val  
 45 50 55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244  
 Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile  
 60 65 70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292  
 Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu  
 75 80 85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat 340  
 Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp  
 90 95 100

tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca 388  
 Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro  
 105 110 115 120

cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca 436



Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser

125 130 135

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Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe

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Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val

155 160 165

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His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr

170 175 180

cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg 628

His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val

185 190 195 200

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676

Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp

205 210 215

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724

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220 225 230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772

Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu

235

240

245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg 820

Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met

250

255

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caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt 868

Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu

265

270

275

280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916

Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys

285

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Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met

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Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr

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Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn

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Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro

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385

390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct 1252

Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser

395

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425

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445

450

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Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly

460

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Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu

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gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att 1540

Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile

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495

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Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val

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510

515

520

aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag 1636

Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln

525

530

535

aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa 1684

Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu

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555

560

565

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Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala

570

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580

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635 640 645

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aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac 2164  
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp

700	705	710	
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Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg			
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Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser			
730	735	740	
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Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val			
745	750	755	760
gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct			2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala			
765	770	775	
gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg			2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu			
780	785	790	
agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga			2452
Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg			
795	800	805	
gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt			2500
Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu			
810	815	820	

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aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596  
 Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile  
 845 850 855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt 2644  
 Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser  
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 His Thr Leu Ser Arg Ser Thr Thr His Leu Ile  
 875 880

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aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717

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atacctaataa ccc

3910



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<212> PRT

<213> Homo sapiens

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Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn

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Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser

35

40

45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg

50

55

60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys

65

70

75

80

Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp

85

90

95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly

100

105

110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His  
115 120 125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu  
130 135 140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln  
145 150 155 160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn  
165 170 175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys  
180 185 190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser  
195 200 205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala  
210 215 220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly  
225 230 235 240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met  
245 250 255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu  
260 265 270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln  
275 280 285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp  
290 295 300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys  
305 310 315 320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg  
325 330 335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu  
340 345 350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe  
355 360 365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile  
370 375 380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly  
385 390 395 400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu  
405 410 415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu

420

425

430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys

435

440

445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly

450

455

460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met

465

470

475

480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His

485

490

495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln

500

505

510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr

515

520

525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln

530

535

540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys

545

550

555

560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr

565

570

575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys  
580 585 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr  
595 600 605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val  
610 615 620

<210> 54

<211> 2426

<212> DNA

<213> Homo sapiens

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Met Glu Gly Pro

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ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163

Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro

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10

15

20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211

Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala

25 30 35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259

Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp

40 45 50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307

Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu

55 60 65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355

Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser

70 75 80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403

Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe

85 90 95 100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451

Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn

105 110 115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499

Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val

120 125 130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547

Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu

135

140

145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595

Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile

150

155

160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643

Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val

165

170

175

180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691

Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro

185

190

195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt 739

Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val

200

205

210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga 787

Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly

215

220

225

aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat 835

Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp

230

235

240

atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac 883

Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn  
245 250 255 260

aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga 931  
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg  
265 270 275

gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc 979  
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu  
280 285 290

ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac 1027  
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr  
295 300 305

ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta 1075  
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu  
310 315 320

gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg 1123  
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly  
325 330 335 340

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt 1171  
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val  
345 350 355

ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca 1219  
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala



360

365

370

gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta 1267

Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu

375

380

385

tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct 1315

Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala

390

395

400

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc 1363

Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly

405

410

415

420

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca 1411

Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro

425

430

435

tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat 1459

Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr

440

445

450

gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507

Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His

455

460

465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555

His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp

470

475

480

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603

Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr

485 490 495 500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651

Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys

505 510 515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699

Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser

520 525 530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747

Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

535 540 545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795

Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His

550 555 560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843

Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe

565 570 575 580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891

Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val

585 590 595

aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939  
 Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His  
 600 605 610

cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989  
 Pro Ala Arg Glu Lys Val Leu Arg Ser Val  
 615 620

ctctcaatct gatttgTTTT tgTTtatgtc gatgccctgt agTTtgaaag tgaagtaaag 2049

atttagaatt cacctaagtc caaaggaaaa cacgtggTTT ttaaagccat taggtaaaaa 2109

aagttctcaa taaaggcatt acaattTTTT aggtTTtagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata tttttcacia gaaaatgcaa gttactTTTT 2229

ttggaaataa tactcactga ttatggataa aatgggaatat tttcagatac tatattggct 2289

gtttcaaaat agtactattc tttaaacttg taatttttgc taagttatTT gtctttgttg 2349

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aaaaaatttt tttttgt 2426

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<212> PRT

<213> Homo sapiens

<400> 55

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Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe

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Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro

35 40 45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu

50 55 60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu

65 70 75 80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly

85 90 95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg

100 105 110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly

115 120 125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly

130 135 140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln  
145 150 155 160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly  
165 170 175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu  
180 185 190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala  
195 200 205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr  
210 215 220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu  
225 230 235 240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp  
245 250 255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10)..(780)

<400> 56

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10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly

15

20

25

30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147

Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg

35

40

45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195

Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala

50

55

60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243

Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe

65

70

75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291

Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr

80

85

90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339

Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr

95 100 105 110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387

Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly

115 120 125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435

Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

130 135 140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483

Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser

145 150 155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531

Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro

160 165 170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579

Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu

175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627

Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile

195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675  
 Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val  
 210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723  
 Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys  
 225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771  
 Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala  
 240 245 250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820  
 Thr Asp Gly  
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actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

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caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

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tgctgtctct gtttctagct ccatggttgg cctgggtggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag 1520

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<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

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Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys

20 25 30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu

35 40 45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe

50 55 60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile  
65 70 75 80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His  
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Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val  
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<210> 58

<211> 1496

<212> DNA

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<221> CDS

<222> (9)..(329)

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atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98

Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys

15

20

25

30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146  
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln  
 35 40 45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194  
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu  
 50 55 60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242  
 Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp  
 65 70 75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290  
 Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met  
 80 85 90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339  
 Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val  
 95 100 105

tttgatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399

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caaaccattc agatcagcca ctgctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaacca ggactcagtc 579

ctgcttcttt tgcctcgagt gattttcctc tgtttttcac taaataagca aatgaaaact 639

ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg ccctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759

gaatgtaa at aaggggcagg tcttggccct agaggattga gatgtttttc tatacttag 819

aactattttt ggataaatta tatattttcc ttcctagtag aagtgttact gcctgtaact 879

agctcaaa at accaatgcag tttctgcatt ctgggttttg tttttctttt tttttttttt 939

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1496

&lt;210&gt; 59

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly

1

5

10

15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp

20

25

30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met

35

40

45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly

50

55

60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln

65

70

75

80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr

85

90

95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr

100

105

110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys  
115 120 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg  
130 135 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu  
145 150 155 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro  
165 170 175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val  
180 185 190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr  
195 200 205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu  
210 215 220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln  
225 230 235 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu  
245 250 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

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Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215

Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20

25

30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263

Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35

40

45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311

Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50

55

60

65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359

Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70

75

80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407

Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85

90

95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455

Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100

105

110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503

Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val

115

120

125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551

Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu

130

135

140

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cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599

Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His

150

155

160



gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647

Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser

165

170

175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu

180

185

190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743

Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr

195

200

205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791

Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met

210

215

220

225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839

His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr

230

235

240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887

Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg

245

250

255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932

Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatittgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgcagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtagct ttcataggat tcttgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgtg gtgaacttca accccaaaat tttaaaaatg tatttcccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

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tcttggtccc tgaatagtc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttgcccat 1832

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg

1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

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15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

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25

30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35

40

45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

50

55

60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp

65

70

75

80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile

85

90

95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly

100

105

110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile

115

120

125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu

130

135

140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu

145

150

155

160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala

165

170

175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile

180

185

190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val

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200

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Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser

210

215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (49)..(705)

<400> 62

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Met Asn Arg

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ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

5

10

15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

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25

30

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tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201

Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys

40

45

50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249

Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg

55

60

65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297

Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala

70

75

80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345

Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu

85

90

95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393

Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu

100

105

110

115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441

Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu

120

125

130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489

Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu

135

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gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537

Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu

150

155

160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585

Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp

165

170

175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633

Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly

180

185

190

195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681

Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe

200

205

210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735

Gly Leu Pro Gln Ile Pro Ala Ser

215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795

ttaggtttct ttcctttctt tgaaggaaag tttaattaca ttgctctttt attttttcca 855

ttaagagact cattgcttgg gaaatgcttt cttcgtacta aaatttgatt cctttttttt 915

cttatgaaaa acgaactcag tttaaaagta ttttttagctc gtatgacttg ttttcattca 975

ttaataataa ttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg 1155

cctttttgat gggttttggt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335

tataactcaat aaatattttt caaaagg

1362

&lt;210&gt; 63

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro

1

5

10

15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly

20

25

30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

35

40

45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg

50

55

60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn

65

70

75

80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val

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90

95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp

100

105

110



Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser  
115 120 125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp  
130 135 140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr  
145 150 155 160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met  
165 170 175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His  
180 185 190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn  
195 200 205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu  
210 215 220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn  
225 230 235 240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys  
245 250 255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln

260

265

270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp

275

280

285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile

290

295

300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile

305

310

315

320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser

325

330

335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile

340

345

350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe

355

360

365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn

370

375

380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro

385

390

395

400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu

405

410

415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys  
420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg  
435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val  
450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu  
465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu  
485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr  
500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser  
515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr  
530 535 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg  
545 550 555 560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe  
565 570 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys  
580 585 590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr  
595 600 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val  
610 615 620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (14)..(1879)

<400> 64

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Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala

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ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97

Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His

15

20

25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145

Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp

30

35

40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193

Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr

45

50

55

60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241

Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro

65

70

75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80

85

90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95

100

105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385

Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln

110

115

120

ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct 433

Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro

125

130

135

140

tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag 481

Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln  
 145 150 155

ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat 529  
 Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp  
 160 165 170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca 577  
 Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala  
 175 180 185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat 625  
 Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn  
 190 195 200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat 673  
 Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His  
 205 210 215 220

tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa 721  
 Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu  
 225 230 235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt 769  
 Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu  
 240 245 250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa 817  
 Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln

255	260	265	
gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag 865			
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys			
270	275	280	
ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct 913			
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro			
285	290	295	300
ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat 961			
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp			
	305	310	315
tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta 1009			
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val			
	320	325	330
cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg 1057			
Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu			
	335	340	345
ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105			
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp			
	350	355	360
ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153			
Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro			
365	370	375	380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201

Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249

Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297

Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415

420

425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345

Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly

430

435

440

gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393

Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val

445

450

455

460

ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441

Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu

465

470

475

ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct 1489

Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser

480

485

490



tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537

Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp

495

500

505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585

Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met

510

515

520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg 1633

Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met

525

530

535

540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681

Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg

545

550

555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729

Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile

560

565

570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777

Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe

575

580

585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825

Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr

590

595

600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873

Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln  
605 610 615 620

ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg cctgaaaatt 1929  
Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169

ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatggt 2229

cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtag 2289

gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt attatgtaca 2349

tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409

ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca atgttttggt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529

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ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649

cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709

ttttaagggt taaggtggtt ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769

taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829

aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889

agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

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<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp

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15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

20

25

30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly

35

40

45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala

50

55

60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly  
65 70 75 80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp  
85 90 95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys  
100 105 110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu  
115 120 125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met  
130 135 140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys  
145 150 155 160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu  
165 170 175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr  
180 185 190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg  
195 200 205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His

210

215

220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val

225

230

235

240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile

245

250

255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp

260

265

270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn

275

280

285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys

290

295

300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile

305

310

315

320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly

325

330

335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His

340

345

350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe

355

360

365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe  
370 375 380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr  
385 390 395 400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr  
405 410 415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser  
420 425 430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val  
435 440 445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp  
450 455 460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg  
465 470 475 480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met  
485 490 495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr  
500 505 510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser  
515 520 525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp  
530 535 540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly  
545 550 555 560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys  
565 570 575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg  
580 585 590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro  
595 600 605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile  
610 615 620

Ser Gly Ser Gly Tyr Gln Leu Val  
625 630

<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

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<222> (108)..(2003)

<400> 66

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cctccgcctc gcccgagccc cgggaggggtg aaacgctttc tcccagc atg cag cgg 116

Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5

10

15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20

25

30

35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40

45

50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308

His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

55

60

65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356

Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70

75

80



cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404

Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85

90

95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452

Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

100

105

110

115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500

Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120

125

130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548

Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135

140

145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596

Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu

150

155

160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165

170

175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692

Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180

185

190

195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740  
 Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu  
 200 205 210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788  
 Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr  
 215 220 225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836  
 Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu  
 230 235 240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884  
 Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu  
 245 250 255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932  
 Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn  
 260 265 270 275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980  
 His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe  
 280 285 290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028  
 Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu  
 295 300 305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076

Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu  
 310 315 320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124  
 Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp  
 325 330 335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172  
 Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His  
 340 345 350 355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat 1220  
 Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr  
 360 365 370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc 1268  
 Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile  
 375 380 385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga 1316  
 His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly  
 390 395 400

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa 1364  
 Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln  
 405 410 415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc 1412  
 Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu

420	425	430	435	
agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa				1460
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys				
	440	445	450	
cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc				1508
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys				
	455	460	465	
cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg				1556
Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met				
	470	475	480	
ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt				1604
Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly				
	485	490	495	
tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat				1652
Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp				
500	505	510	515	
gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg				1700
Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met				
	520	525	530	
ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta				1748
Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val				
	535	540	545	

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796

Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr

550

555

560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844

Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr

565

570

575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892

Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile

580

585

590

595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940

Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val

600

605

610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988

Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615

620

625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg 2043

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

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caagttcact gcatgtctga tgcttggttaa aactagtctt ccctgtaaaa tgcagattac 3603

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gcatatgtac ttattttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattgggtt aactttacaa atgtcagcta gttttgacta 3903

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aatacatttt tatcaacagt taaagactat ggtgggtttt tcagagtttg gctaagaatg 4083

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ggagccagct atgcagcagt ataccatctg tttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aaccagttc taaagtgtg tatgatggcg aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagttttttt tcattcatat ttttgttggt tccaggaatt tatttgatat 4503

taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatatttc 4563

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taaaatatta atcagaataa atactgactc tt 4715



<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

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Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20

25

30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35

40

45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50

55

60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65

70

75

80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100

105

110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115

120

125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg  
130 135 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln  
145 150 155 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp  
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly  
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln  
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn  
210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile  
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala  
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val  
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr

275

280

285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro

290

295

300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu

305

310

315

320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu

325

330

335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu

340

345

350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr

355

360

365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr

370

375

380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser

385

390

395

400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser

405

410

415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe

420

425

430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu  
 435 440 445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln  
 450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp  
 465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe  
 485 490 495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

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<222> (22)..(1515)

<400> 68

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His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339

Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

145

150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155

160

165

170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

180

185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

210

215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723

Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220

225

230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu  
235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819  
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala  
255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867  
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys  
270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915  
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp  
285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963  
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro  
300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011  
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu  
315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059  
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly  
335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107  
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350	355	360	
cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca			1155
His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser			
365	370	375	
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc			1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly			
380	385	390	
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac			1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp			
395	400	405	410
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc			1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg			
415	420	425	
tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc			1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile			
430	435	440	
tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta			1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu			
445	450	455	
cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca			1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala			
460	465	470	



aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491  
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser  
475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat 1545  
Gln Lys Leu Trp Glu Phe Ser Cys  
495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat ttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc ttgtttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845

atttcctagg agttgggttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1

5

10

15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20

25

30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35

40

45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50

55

60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65

70

75

80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100

105

110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115

120

125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp  
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly  
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln  
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn  
210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile  
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala  
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val  
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr  
275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro  
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu  
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu  
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu  
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr  
355 360 365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr  
370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser  
385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser  
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe  
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu  
435 440 445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln  
450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465                      470                      475                      480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe

485                      490                      495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1                      5                      10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15                      20                      25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30

35

40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45

50

55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60

65

70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75

80

85

90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339

Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95

100

105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110

115

120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

145

150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190 195 200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205 210 215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723

Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220 225 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819

Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867  
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys  
270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915  
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp  
285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963  
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro  
300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011  
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu  
315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059  
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly  
335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107  
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr  
350 355 360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155  
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser  
365 370 375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203



Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly  
380 385 390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251  
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp  
395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299  
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg  
415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347  
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile  
430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395  
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu  
445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443  
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala  
460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491  
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser  
475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttgggta gttttactgt aattttctat 1545  
Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttgtt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His

1

5

10

15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr

20

25

30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr

35

40

45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro  
50 55 60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly  
65 70 75 80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro  
85 90 95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp  
100 105 110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr  
115 120 125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala  
130 135 140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu  
145 150 155 160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys  
165 170 175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly  
180 185 190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val

195

200

205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg

210

215

220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly

225

230

235

240

Gln Trp Ile Gln Arg

245

<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)..(861)

<400> 72

ggaagtcggc caccttcctc cgtcccggcc gttagcccag ccaagcccag ccaagcccag 60

ccaagccccg ccgatacgcg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1

5

10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216  
Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser  
15 20 25 30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264  
Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile  
35 40 45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312  
Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His  
50 55 60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360  
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg  
65 70 75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408  
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser  
80 85 90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456  
Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile  
95 100 105 110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504  
Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe  
115 120 125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552  
 Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys  
 130 135 140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600  
 Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu  
 145 150 155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648  
 Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn  
 160 165 170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696  
 Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile  
 175 180 185 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744  
 Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly  
 195 200 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792  
 Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile  
 210 215 220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840  
 Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val  
 225 230 235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891

Leu Gly Gln Trp Ile Gln Arg

240

245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggtctg tgaacgaggc ctgtctcttc cctggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggctg 1071

ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagaccagg 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gcccgaagtc tgttctgact ttgcctggct gtctccttga 1251

ccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311

tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccc gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491

gattgtgttc ctccctatg ggatccatct gttttgtaaa caataaagcg tctgaggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly  
1 5 10 15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys  
20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly  
35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro  
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn  
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu  
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp  
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu  
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro  
130 135 140



Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His  
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly  
165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly  
180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val  
195 200 205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln  
210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp  
225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe  
245 250 255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu  
260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser  
275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

290

295

300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val

305

310

315

320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

325

330

335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

340

345

350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 74

ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val  
5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210  
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser  
25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258  
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys  
40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306  
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile  
55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354  
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val  
70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402  
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys  
85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450  
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile  
105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498  
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120	125	130	
gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg			546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val			
135	140	145	
gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag			594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln			
150	155	160	
tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa			642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys			
165	170	175	180
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca			690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr			
185	190	195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg			738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro			
200	205	210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc			786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser			
215	220	225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg			834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala			
230	235	240	

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882

Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg

245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930

Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln

265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978

Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325 330 335 340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345 350

gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctggggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgccttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcagggtcaa cttgtgttcc 1708

tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1

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10

15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20

25

30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35

40

45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro  
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn  
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu  
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp  
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu  
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro  
130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His  
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly  
165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly  
180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val  
195 200 205



Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln  
210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp  
225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe  
245 250 255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu  
260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser  
275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val  
290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val  
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys  
325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser  
340 345 350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 76

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tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile  
 55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354  
 Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val  
 70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402  
 Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys  
 85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450  
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile  
 105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498  
 Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu  
 120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546  
 Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val  
 135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594  
 Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln  
 150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642  
 Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165	170	175	180	
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca				690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr				
	185	190	195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg				738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro				
	200	205	210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc				786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser				
	215	220	225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg				834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala				
	230	235	240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg				882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg				
245	250	255	260	
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag				930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln				
	265	270	275	
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct				978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro				
	280	285	290	

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

345

350

gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

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caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tggttttttc tggtgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcagggtcaa cttgtgttcc 1708

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tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala

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10

15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20

25

30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35

40

45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile

50

55

60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile

65

70

75

80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn

85

90

95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser

100

105

110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu  
115 120 125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser  
130 135 140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu  
145 150 155 160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys  
165 170 175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile  
180 185 190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe  
195 200 205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile  
210 215 220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp  
225 230 235 240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu  
245 250 255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met  
260 265 270



Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr  
 275 280 285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe  
 290 295 300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His  
 305 310 315 320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp  
 325 330 335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe  
 340 345 350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala  
 355 360 365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser  
 370 375 380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe  
 385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile  
 405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu

420

425

430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu

435

440

445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly

450

455

460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys

465

470

475

480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp

485

490

495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp

500

505

510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp

515

520

525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu

530

535

540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn

545

550

555

560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp

565

570

575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp  
580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys  
595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp  
610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met  
625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp  
645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys  
660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr  
675 680 685

Gly Gln Gly Phe Lys Leu Val Lys Ser  
690 695

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372)..(2462)

<400> 78

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcggggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctgggta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

1

5

10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458

Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met

15

20

25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506

His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu

30

35

40

45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554

Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn

50

55

60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602

Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile

65

70

75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650

Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser

80

85

90

ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698

Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu

95

100

105

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746

Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr

110

115

120

125

ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794

Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu

130

135

140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt 842

Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val

145

150

155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890  
 Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu  
 160 165 170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938  
 Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met  
 175 180 185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986  
 Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu  
 190 195 200 205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034  
 Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys  
 210 215 220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082  
 Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro  
 225 230 235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130  
 Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys  
 240 245 250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt 1178  
 Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe  
 255 260 265

gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt 1226

Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu  
270 275 280 285

aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt 1274  
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe  
290 295 300

gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg 1322  
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp  
305 310 315

gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac 1370  
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His  
320 325 330

agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg 1418  
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met  
335 340 345

cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt 1466  
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu  
350 355 360 365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514  
Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile  
370 375 380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562  
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His

385

390

395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610

Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly

400

405

410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658

Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro

415

420

425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706

Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr

430

435

440

445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754

Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu

450

455

460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802

Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu

465

470

475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc 1850

His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro

480

485

490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898

Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr

495

500

505



gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt 1946

Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu

510

515

520

525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att 1994

Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile

530

535

540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042

Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg

545

550

555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090

Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys

560

565

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aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138

Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

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aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp

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act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234

Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg

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620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282

Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys

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cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330

His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu

640

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gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378

Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys

655

660

665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426

Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val

670

675

680

685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttgac 2472

Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

690

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cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttgga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggtcaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832

gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892

cttttttcca aacagtaggt ttcaccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaatit gcttatactc catcac 3008

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<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

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1 5 10 15

Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val

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Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg

35 40 45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg

50 55 60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala

65

70

75

80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu

85

90

95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser

100

105

110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe

115

120

125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe

130

135

140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu

145

150

155

160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys

165

170

175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe

180

185

190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val

195

200

205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile

210

215

220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys  
225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg  
245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln  
260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser  
275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu  
290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys  
305 310 315 320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe  
325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln  
340 345 350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe  
355 360 365

Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser  
370 375 380

Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu  
385 390 395 400

Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr  
405 410 415

Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp  
420 425 430

Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly  
435 440 445

Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr  
450 455 460

Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val  
465 470 475 480

Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro  
485 490 495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn  
500 505 510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala  
515 520 525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro

530

535

540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile

545

550

555

560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu

565

570

575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met

580

585

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Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu

595

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Val Lys Ser

610

<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (629)..(2461)

<400> 80

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcactgcgtt attgcttttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatcttg 480

ctatttagcc agaatcaatt tattggttgc tataatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

1

5

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700

Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp

10

15

20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748

Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu



25

30

35

40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796

Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg

45

50

55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844

Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu

60

65

70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892

Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val

75

80

85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940

Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu

90

95

100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988

Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val

105

110

115

120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036

Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn

125

130

135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084

Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe

140

145

150

ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc 1132

Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro

155

160

165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180

Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala

170

175

180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228

Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg

185

190

195

200

gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga 1276

Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly

205

210

215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324

Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly

220

225

230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372

Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg

235

240

245

aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc 1420

Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg

250

255

260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca 1468  
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala  
265 270 275 280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc 1516  
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe  
285 290 295

ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg 1564  
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly  
300 305 310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612  
Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr  
315 320 325

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660  
Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr  
330 335 340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708  
Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly  
345 350 355 360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756  
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr  
365 370 375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804

Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His  
 380 385 390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852  
 Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg  
 395 400 405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900  
 His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly  
 410 415 420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948  
 Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile  
 425 430 435 440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996  
 Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile  
 445 450 455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044  
 Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys  
 460 465 470

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca 2092  
 Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr  
 475 480 485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140  
 Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

490

495

500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188

Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr

505

510

515

520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg 2236

Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp

525

530

535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284

Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His

540

545

550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332

Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala

555

560

565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380

Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe

570

575

580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428

Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu

585

590

595

600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481

Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

605

610

gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgctgta 2541

tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661

agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa tggatcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901

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<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

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Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln  
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Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys  
35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln  
50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser  
65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu  
85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro  
100 105 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys  
115 120 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser  
130 135 140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile  
145 150 155 160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro  
165 170 175

Thr Glu Met Asp Glu Asn Glu Ser

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<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (285)..(836)

<400> 82

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ccgcacccccg gggctcacac ttacccgcgc ggaggagcag cggccgggtg tccacccccca 180

tcctgcgcc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag cccaggtgg gccttgtgca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val



5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55

60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70

75

80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85

90

95

100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg 632

Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met

105

110

115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag 680

Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu

120

125

130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc 728

Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu

135

140

145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc 776

Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly

150

155

160

act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat 824

Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp

165

170

175

180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa 876

Glu Asn Glu Ser

gagctctgta gatgctgtat agacactaaa taagagtga ttagggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996

ttagtcatta acttagtcac ctgttgatt ctggatctac acaaaattat tttaactgct 1056

cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tcgtgttctc 1116

aaaataaggt tatattattt tctttttctg cttgattttc atcttgtgtt ttgctttgtt 1176

tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236

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gagaaatact accttacttt tctatgattt ctttttacag agttatagtg tgtttactcc 1416

taagatgaca gttctctttg tctatatcca gcatctaaga caaatattta aacattttta 1476

agaaccactg tgtaagttt aggattattt acttaccaaa ttagaagttt gacttttatg 1536

tggtatacac aatcttaaaa tttcacgaat tcaccttttt aatagtatcc atgtacataa 1596

taaaatcaaa gtttaattag c 1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro  
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu  
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val  
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser  
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg  
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln  
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser  
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser  
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305

310

315

320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325

330

335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340

345

350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

Val Glu Ser Pro Val Gln Lys Val

385

390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1294)

<400> 84

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atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

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25

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cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

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45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

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55

60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245 250 255



agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934  
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu  
 260 265 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982  
 Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr  
 275 280 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030  
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu  
 290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078  
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly  
 305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126  
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala  
 325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174  
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val  
 340 345 350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222  
 Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg  
 355 360 365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro  
 370 375 380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324  
 Val Glu Ser Pro Val Gln Lys Val  
 385 390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgaggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

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gagccccggg ggtagacagt cctcagttag gggttttggg gagtttgggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624

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aaagcacaag cggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgcca gcaccaccac ctccatgct cctggatccc 1804

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta actttttgct 1864

cttataattt tattttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr  
20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser  
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro  
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu  
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val  
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser  
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg  
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln  
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser  
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser  
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met  
210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr  
225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser  
245 250 255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu  
260 265 270

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp  
275 280 285

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe  
290 295 300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu  
305 310 315 320

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu  
325 330 335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln  
340 345 350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr  
355 360 365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu  
370 375 380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val  
385 390 395 400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys  
405 410 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val  
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<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (119)..(1414)

<400> 86

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atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

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25

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cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

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ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

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60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694  
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser  
 180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742  
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser  
 195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790  
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met  
 210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838  
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr  
 225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886  
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser  
 245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934  
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu  
 260 265 270

atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg 982  
 Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp  
 275 280 285

cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt 1030



Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe  
 290 295 300

ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa 1078  
 Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu  
 305 310 315 320

cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag 1126  
 Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu  
 325 330 335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag 1174  
 Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln  
 340 345 350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc 1222  
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr  
 355 360 365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270  
 Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu  
 370 375 380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318  
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val  
 385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366  
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405

410

415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

420

425

430

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gcaccaccac ctccatgct cctggatccc taggtctgtg tccatgagcc tgttgcaggt 1954

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ctgc

2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser  
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Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser  
20 25 30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His  
35 40 45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser  
50 55 60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys  
65 70 75 80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val  
85 90 95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe  
100 105 110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala  
115 120 125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu  
130 135 140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser  
145 150 155 160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu  
165 170 175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile  
180 185 190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg  
195 200 205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu  
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Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala  
225 230 235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (111)..(815)

<400> 88

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aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

5

10

15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212

Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

20

25

30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260

Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn

35

40

45

50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308

Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu

55

60

65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356

Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val

70

75

80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404

Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn

85

90

95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452

Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu

100

105

110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500

Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn

115

120

125

130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat 548

Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp

135

140

145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596

Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn

150

155

160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644

Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

165

170

175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692

Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

180

185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740  
 Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe  
 195 200 205 210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788  
 Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg  
 215 220 225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835  
 Asn Met Val Gln Arg Gln Phe Ile Ala  
 230 235

gtggctggct cttgttttgt aaaccaaagt attaattctt acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

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ggaatttctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

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aagactttgg atagaaggag atgtatttta ttacctccta ttctagagcc ccatgctcct 1795

aacaagccag agaggcccca aacaggattg tttcttttct ccacagccct tctgcccac 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggatcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975

ctgaggatga atgtaactgt gggcaaacta tttaccctcc tttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac 2095

cacaaaaggg aacaagcaaa aaagtttgga ttcgataaag tgatatgtaa tagttgcaga 2155

aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215



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tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515

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agtattcatt tttttgcat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635

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aaaataaatg tttttattct tt 2717

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<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20

25

30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35

40

45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50

55

60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65

70

75

80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85

90

95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100

105

110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115

120

125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130

135

140

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145

150

155

160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

165

170

175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val  
 180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu  
 195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu  
 210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn  
 225 230 235 240

Gln Tyr Glu Ile Val  
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<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (60)..(794)

<400> 90

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atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys  
1 5 10 15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155  
Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly  
20 25 30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203  
Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn  
35 40 45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251  
Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu  
50 55 60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299  
Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe  
65 70 75 80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347  
Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe  
85 90 95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395  
Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe  
100 105 110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443  
Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115

120

125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130

135

140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145

150

155

160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

165

170

175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180

185

190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195

200

205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210

215

220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225

230

235

240

cag tat gag ata gtg taaccaatg tatctgtggg cctattcctc tctaccttta 834

Gln Tyr Glu Ile Val

245

aggacattta gggcccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

atcaagatgt atgtttgcta tgttctaagt ccaccttcta tccattcat gttagatcgt 1074

tgaaaccctg tatccctctg aaacactgga agagctagta aattgtaaata gaagtaatac 1134

tgtgttcctc ttgactgtta tttttcttag tagggggcct ttggaaggca ctgtgaattt 1194

gctattttga tgtagtgta caagatggaa aattgattcc tctgactttg ctattgatgt 1254

agtgtgatag aaaattcacc cctctgaact ggctccttcc cagtcaaggt tatctggttt 1314

gattgtataa ttgacacaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374

cagagagtca cattgtgtaa ttttaatttca gtcagtcaat agatggcatc cctcatcagg 1434

gttgccagat ggtgataaca gtgtaaggcc ttgggtctaa ggcattccacg actggaaggg 1494

actactgatg ttctgtgata catcaggttt cagcacacaa cttacatttc ttgcctcca 1554

aattgaggca tttattatga tgttcataact ttccctcttg tttgaaagtt tctaattatt 1614

aatggtgtc ggaattgttg tattttcctt aggaattcag tggaacttat cttcattaaa 1674

tttagctggt accaggttga tatgacttgt caatattatg gtcaacttta agtcttagtt 1734

ttcgtttggt cctttgatta ataagtataa ctcttataca ataaatactg ctttcctct 1793

<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

1 5 10 15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu

20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala

35 40 45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

50 55 60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

65 70 75 80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85

90

95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

100

105

110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115

120

125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130

135

140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

145

150

155

160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

165

170

175

Ala Leu Leu Gln

180

<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>



<221> CDS

<222> (26)..(565)

<400> 92

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Met Ala Ser Thr Ser Tyr Asp Tyr Cys

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aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 100

Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly

10

15

20

25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148

Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

30

35

40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196

Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45

50

55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244

Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

60

65

70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292

Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala

75

80

85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340

Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu  
90 95 100 105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388  
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr  
110 115 120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436  
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu  
125 130 135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484  
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr  
140 145 150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532  
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu  
155 160 165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585  
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln  
170 175 180

acatcttgga aggtccgtcc tgctcggtt ttcgcttgaa cattcccttg atctcatcag 645

ttctgagcgg gtcattggggc aacacggtta gcggggagag cacggggtag ccggagaagg 705

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

ttgacccagg gctgtctccc tccagagcct ccctccggac aatgagtcac ccctcttgtc 825

tcccaccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttggttatg 885

ggtttttttt gcgggggggg ttgctttttt ctgggggtctt tgagctccaa aaaataaaca 945

cttcctttga gggagagcac acctt 970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe

1

5

10

15

Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn

20

25

30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu

35

40

45

Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala

50

55

60

Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp

65

70

75

80

Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile

85 90 95

Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly

100 105 110

Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly

115 120 125

Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr

130 135 140

Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala

145 150 155 160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser

165 170 175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu

180 185 190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser

195 200 205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile

210 215 220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr

225	230	235	240
Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala			
	245	250	255
Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr			
	260	265	270
Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu			
	275	280	285
Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu			
	290	295	300
Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln			
305	310	315	320
Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His			
	325	330	

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(1167)

<400> 94

attatgcaga tgcacggctg gaggtgggat ccacacagct cagaacagct ggatcttgct 60

cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

5

10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

20

25

30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

35

40

45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369

Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile

50

55

60

65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417

Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe

70

75

80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465

Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu

85

90

95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc 513

Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys

100

105

110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc 561

Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile

115

120

125

atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt 609

Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser

130

135

140

145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg 657

Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val

150

155

160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca 705

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala

165

170

175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753

Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys

180

185

190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801

Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu

195

200

205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849

Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg

210

215

220

225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897

Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp

230

235

240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945

Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly

245

250

255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993

Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr

260

265

270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041

Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser

275

280

285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089

Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg

290

295

300

305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137



Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile

310

315

320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc 1187

Tyr Gln Arg Leu Asn Pro Cys His Thr His

325

330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgtagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggctc cactaccgac ctgccccgg ttcgatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtcccctgcc ctgtctttcc agcatccact 1667

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cttgaaccct gaaggccagg taatgagcca tggccattgt ccccagctga ggaccaggtg 1847

tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccatcctgct gagtgccctg tgtgtaagtc ctaataaact 2027

cacctactca cc 2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1 5 10 15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20 25 30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35 40 45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50 55 60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65 70 75 80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145

150

155

160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165

170

175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195

200

205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210

215

220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys

225	230	235	240
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg			
	245	250	255
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu			
	260	265	270
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp			
	275	280	285
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly			
	290	295	300
Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu			
305	310	315	320
Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu			
	325	330	335
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser			
	340	345	350
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser			
	355	360	365
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu			
370	375	380	

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe  
385 390 395 400

Val Cys Lys Tyr Lys Leu Leu  
405

<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181)..(1401)

<400> 96

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tttgccttgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1

5

10

15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20

25

30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35

40

45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50

55

60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65

70

75

80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145 150 155 160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165 170 175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca 756

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180 185 190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195 200 205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc 852

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210 215 220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa 900

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys

225 230 235 240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg

245 250 255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu

260

265

270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp

275

280

285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly

290

295

300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu

305

310

315

320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu

325

330

335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser

340

345

350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

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gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332



Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu  
370 375 380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380  
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe  
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<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

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His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser  
35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala  
50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu  
65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His  
85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys  
100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu  
115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val  
130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser  
145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg  
165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu  
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr  
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg

275

280

285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

325

330

335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

340

345

350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

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360

365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr  
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro  
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu  
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys  
420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro  
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Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly  
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Asp  
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<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

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<222> (477)..(1871)

<400> 98

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ccttggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctaccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agagggtgcag gtgagggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

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55

60

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ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

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75

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gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

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90

95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

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105

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cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr

130

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140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr  
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gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007  
 Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln  
 165 170 175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055  
 Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu  
 180 185 190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103  
 Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu  
 195 200 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151  
 Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu  
 210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199  
 Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala  
 230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247  
 Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala  
 245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295  
 Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

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265

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tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343

Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275

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285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391

His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

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att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310

315

320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487

Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

330

335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535

Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340

345

350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

355

360

365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

375

380

385



agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

390

395

400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

405

410

415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

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465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag

1940

<210> 99

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<213> Homo sapiens

<400> 99

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His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser  
35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala  
50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu  
65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His  
85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys  
100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu  
115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val  
130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser  
145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg  
165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu  
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr  
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn  
210 215 220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser  
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp  
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr  
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg  
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

325

330

335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

340

345

350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

355

360

365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr

370

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380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro

385

390

395

400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu

405

410

415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys

420

425

430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

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Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

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Asp

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<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 100

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ccttggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcattcccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

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gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

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25

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agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

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aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

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ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

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gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

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gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

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105

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cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

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170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103

Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

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agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151  
 Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu  
 210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199  
 Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala  
 230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247  
 Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala  
 245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295  
 Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met  
 260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343  
 Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser  
 275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391  
 His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu  
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att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439  
 Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu  
 310 315 320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487



Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

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Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

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ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

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365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

375

380

385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

390

395

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tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

405

410

415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataatccca 1931

taagggcag

1940

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys

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5

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Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys

20

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Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln

35

40

45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His

50

55

60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys  
65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys  
85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile  
100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp  
115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln  
130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu  
145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val  
165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly  
180 185 190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu  
195 200 205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe  
210 215 220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile  
225 230 235 240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly  
245 250 255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr  
260 265 270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr  
275 280 285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu  
290 295 300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu  
305 310 315 320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln  
325 330 335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro  
340 345 350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala  
355 360 365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr

370

375

380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His

385

390

395

400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr

405

410

415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr

420

425

430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile

435

440

445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu

450

455

460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg

465

470

475

480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln

485

490

495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn

500

505

510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu

515

520

525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val  
530 535 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp  
545 550 555 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser  
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val  
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser  
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn  
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu  
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg  
645 650 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg  
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Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn  
675 680 685

<210> 102  
 <211> 2783  
 <212> DNA  
 <213> Homo sapiens

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 <222> (128)..(2182)

<400> 102

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cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

1 5 10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

15 20 25 30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct ca'g 265

Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln

35 40 45

tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313

Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His

50

55

60

tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361

Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr

65

70

75

ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409

Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala

80

85

90

aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca 457

Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala

95

100

105

110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505

Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys

115

120

125

att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta 553

Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val

130

135

140

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601

Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu

145

150

155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649

Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg



160

165

170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697

Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val

175

180

185

190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745

Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu

195

200

205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

210

215

220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841

Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

225

230

235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889

Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys

240

245

250

caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg 937

Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met

255

260

265

270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985

Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys

275

280

285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033

Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser

290

295

300

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081

Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn

305

310

315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt 1129

Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe

320

325

330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca 1177

Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr

335

340

345

350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225

Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys

355

360

365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273

Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile

370

375

380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321

Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu

385

390

395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369

Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His

400

405

410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417

Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser

415

420

425

430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465

Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg

435

440

445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513

Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys

450

455

460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561

Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val

465

470

475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609

Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys

480

485

490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac 1657

Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr

495

500

505

510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt 1705

Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly  
515 520 525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa 1753  
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys  
530 535 540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca 1801  
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala  
545 550 555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac 1849  
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr  
560 565 570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct 1897  
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro  
575 580 585 590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta 1945  
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu  
595 600 605

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag 1993  
Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln  
610 615 620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041  
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn

625

630

635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089

Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr

640

645

650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137

Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys

655

660

665

670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182

Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675

680

685

tgaaagactt ttcgaatgga ccctatggga ctccctctttt ccactgtgag atctacaggg 2242

aacccaaaag aatgatctag agtatgttga agaagatgga catgtgggtgg tacgaaaaca 2302

attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362

actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttataaa 2422

ggtttttcag acaattttgc agaaaggtgc attgattcct aaattctctc tgttgagagc 2482

atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaaggagg 2542

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ctatggccat atataatttt ttttcattaa tttttgaaga tacttgtggc tggaaaagtg 2662

cattccttgt taataaactt tttattttatt acagcccaaa gagcagtatt tattatcaaa 2722

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g 2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala  
1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr  
20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val  
35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln  
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr  
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys

85

90

95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly

100

105

110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile

115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

130

135

140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

145

150

155

160

Leu

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 104

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ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50

55

60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65

70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met

80

85

90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110



gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447

Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495

Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga gggtctgccc tgggtggtctc 652

acctctccag ggggcccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac gggtttcctgc ctccctgaga ccctgagttc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagttg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcctt tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttgggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaa gagatggggg cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala  
1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr  
20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val  
35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln  
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr  
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys  
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly  
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile  
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val  
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg  
145 150 155 160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 106

ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255  
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr  
 50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303  
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr  
 65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351  
 Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met  
 80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399  
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn  
 95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447  
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly  
 115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495  
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln  
 130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543  
 Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr  
 145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga gggtctgccc tgggtggtctc 652

acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712

aatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

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tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

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tgccagatct tcagtgcacc ttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct ttggtctga aatactttcg aacagaattt ctttttttta 1372

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tggtgtcatt ttcccatgtg ccaatgtagt ctcactt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val

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Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val

20 25 30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys

35 40 45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn

50 55 60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu

65 70 75 80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met

85 90 95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val

100 105 110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys

115 120 125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro

130 135 140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro

145 150 155 160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met

165 170 175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu

180 185 190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His

195 200 205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val

210 215 220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile



225

230

235

240

Gly Phe Phe Leu Gly Lys Phe Ile Leu

245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(978)

<400> 108

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gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237

Met Ala

1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

35

40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys

100

105

110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621

Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe

115

120

125

130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669

Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys

135

140

145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717

Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro

150

155

160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765

His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu

165

170

175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813

Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg

180

185

190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861

His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp

195

200

205

210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909

Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser

215

220

225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957

Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe

230

235

240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt 1008

Phe Leu Gly Lys Phe Ile Leu

245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tgttatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatcccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgccctttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tggttgactga gtttttcac cttacaatcc tgtcccatgg 1548

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<210> 109

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<212> PRT

<213> Homo sapiens

<400> 109

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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

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Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu

115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145                      150                      155                      160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165                      170                      175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180                      185                      190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu

195                      200                      205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg

210                      215                      220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala

225                      230                      235                      240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His

245                      250                      255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu

260                      265                      270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln

275                      280                      285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro

290                      295                      300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser  
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu  
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly  
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys  
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys  
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala  
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg  
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu  
420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg  
435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu  
450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp  
465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val  
485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly  
500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly  
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Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu  
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<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (102)..(1721)

<400> 110

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Met Gly Thr Thr Ala

1 5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10 15 20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25 30 35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40 45 50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55 60 65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70 75 80 85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90 95 100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150

155

160

165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

220

225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

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ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

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aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310

315

320

325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330

335

340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

345

350

355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

360

365

370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375

380

385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390

395

400

405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu

410

415

420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

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att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

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ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

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aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln  
20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser  
35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln  
50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser  
65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu  
85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro  
100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu  
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130

135

140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145

150

155

160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165

170

175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180

185

190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu

195

200

205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg

210

215

220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala

225

230

235

240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His

245

250

255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu

260

265

270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln

275

280

285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro  
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser  
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu  
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly  
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys  
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys  
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala  
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg  
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu  
420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg  
435 440 445



Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu  
 450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp  
 465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val  
 485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly  
 500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly  
 515 520 525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu  
 530 535 540

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 <211> 1810  
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 <222> (102)..(1721)

<400> 112

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Met Gly Thr Thr Ala

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aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

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gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

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ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

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agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

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gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

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160

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ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

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ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

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225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

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cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310

315

320

325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330

335

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gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

345

350

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aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

360

365

370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375

380

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cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390

395

400

405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu

410

415

420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

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Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro  
440 445 450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508  
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile  
455 460 465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556  
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu  
470 475 480 485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604  
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile  
490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652  
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala  
505 510 515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700  
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser  
520 525 530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751  
Thr Ser Glu Pro Lys Glu Glu  
535 540

tggggggaac cccaccctgc cccaccctgc tgaacactca ttacactaaa cacctcttg 1810

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<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

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20 25 30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu  
35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val  
50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu  
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val  
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu  
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

115

120

125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys

130

135

140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu

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155

160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile

165

170

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Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys

180

185

190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile

195

200

205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn

210

215

220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val

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235

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Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro

245

250

255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser

260

265

270



Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu  
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln  
290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met  
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp  
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu  
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser  
355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile  
370 375 380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (201)..(1346)

<400> 114

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aacagcagcg gagtttttaa ctttaaatac acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

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gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

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gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

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gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

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ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

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cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

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tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95

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105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110

115

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gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125

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gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

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atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

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165

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atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175

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aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro  
 190 195 200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857  
 Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val  
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tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905  
 Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly  
 220 225 230 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953  
 Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser  
 240 245 250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001  
 Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr  
 255 260 265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049  
 Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro  
 270 275 280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097  
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg  
 285 290 295

aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145  
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala

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305

310

315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193

Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

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gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350

355

360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg 1926

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe  
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Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu  
35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val  
50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu  
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val  
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu  
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys  
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys  
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu  
145 150 155 160



Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile  
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys  
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile  
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn  
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val  
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro  
245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser  
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu  
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln  
290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

320

335

350

365

380

aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

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gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

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gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

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gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

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ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

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70

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cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

80

85

90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95

100

105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110

115

120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125

130

135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140

145

150

155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

160

165

170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175

180

185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

190

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acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

205

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tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905  
 Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly  
 220 225 230 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953  
 Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser  
 240 245 250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001  
 Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr  
 255 260 265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049  
 Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro  
 270 275 280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097  
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg  
 285 290 295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145  
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala  
 300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193  
 Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His  
 320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

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345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

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tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

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ctg gag atc tagatacagg ctgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

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ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cgggtggaggt 1446

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<212> PRT

<213> Homo sapiens

<400> 117

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20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln



35

40

45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50

55

60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65

70

75

80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85

90

95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100

105

110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115

120

125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130

135

140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala

145

150

155

160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165

170

175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180

185

190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu  
195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr  
210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala  
225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu  
245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr  
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg  
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro  
290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg  
305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr  
325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu  
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

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Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385

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Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

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60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687

Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

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ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735

Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205

210

215

220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783

Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr

225

230

235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831

Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys

240

245

250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879

Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu

255

260

265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927

Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg

270

275

280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975

Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser

285

290

295

300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023

Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu

305

310

315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071

Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly

320

325

330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119

Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu  
365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263  
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln  
385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319  
Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccagggt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatggg cccctgccct gtctttccag catccactct 1679

cccttgctct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcggttg 1739

ggtggttgct atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtgggtg agccatggcc atgggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

1 5 10 15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65 70 75 80



Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly  
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg  
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn  
115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe  
130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala  
145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn  
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val  
180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu  
195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr  
210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala  
225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu  
245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr  
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg  
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro  
290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg  
305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr  
325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu  
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala  
355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile  
370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385

390

395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687

Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735

Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205

210

215

220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783

Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr

225

230

235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831

Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys

240

245

250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879

Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu

255

260

265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927

Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg

270

275

280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975  
 Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser  
 285 290 295 300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023  
 Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu  
 305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071  
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly  
 320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119  
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp  
 335 340 345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167  
 Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys  
 350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215  
 Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu  
 365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263  
 Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln  
 385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319

Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatggc cccctgccct gtctttccag catccactct 1679

cccttgctct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

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acactgaagg gcaggtgggtg agccatggcc atgggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcac

2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1

5

10

15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20

25

30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35

40

45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50

55

60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65

70

75

80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

85

90

95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu

100

105

<210> 122



<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(412)

<400> 122

actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc 60

gcccgcgccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc 112

Met Gly Val Gln Val Glu Thr Ile

1

5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160

Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val

10

15

20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208

Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser

25

30

35

40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256

Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304

Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352

Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400

Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tgttcttgga 452

Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tcccctttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatattt gttttcattt tgggggtgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatgggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attggtgttg gggggggggg ttgcaagaat 812

attttatattt aattttttgg atgaaattt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

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gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa cttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtga agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggatcatgc agcttcagca 1352

tctcctgttt ttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagcccctt ctcaccctt tgctgtcctg tgtagtgatt tggtagagaaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgcctta 1532

tgccggcttt tctc 1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly

1 5 10 15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala

20 25 30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe

35 40 45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile

50 55 60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys

65 70 75 80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn

85 90 95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly

100 105 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser

115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala

130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met

145	150	155	160
Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu			
	165	170	175
Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro			
	180	185	190
Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile			
	195	200	205
Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp			
	210	215	220
Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val			
	225	230	235
			240
Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg			
	245	250	255
Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met			
	260	265	270
Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser			
	275	280	285
Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala			
	290	295	300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys  
305 310 315 320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val  
325 330 335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val  
340 345 350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn  
355 360 365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp  
370 375 380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val  
385 390 395 400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn  
405 410 415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser  
420 425 430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu  
435 440 445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr  
450 455 460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile  
465 470 475 480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser  
485 490 495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser  
500 505 510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe  
515 520 525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala  
530 535 540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr  
545 550 555 560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu  
565 570 575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr  
580 585 590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu  
595 600 605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His

610

615

620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys

625

630

635

640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val

645

650

655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe

660

665

670

Arg Tyr Val Ile Leu Arg Met

675

<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala



1

5

10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15

20

25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30

35

40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45

50

55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60

65

70

75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80

85

90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401

Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95

100

105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449

Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110

115

120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497

Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125

130

135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545

Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140

145

150

155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593

Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160

165

170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641

Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175

180

185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689

Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala

190

195

200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737

Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro

205

210

215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg 785

Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser

220

225

230

235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt 833  
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys  
240 245 250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct 881  
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser  
255 260 265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa 929  
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu  
270 275 280

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct 977  
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser  
285 290 295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025  
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg  
300 305 310 315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073  
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu  
320 325 330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc 1121  
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr  
335 340 345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt 1169

Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser  
350 355 360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac 1217  
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His  
365 370 375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta 1265  
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu  
380 385 390 395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc 1313  
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro  
400 405 410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc 1361  
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly  
415 420 425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa 1409  
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu  
430 435 440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457  
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile  
445 450 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505  
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His

460

465

470

475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553

Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly

480

485

490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601

Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp

495

500

505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649

Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala

510

515

520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697

Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile

525

530

535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745

Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser

540

545

550

555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793

Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly

560

565

570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841

Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met

575

580

585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889

Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu

590

595

600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937

Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro

605

610

615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985

Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp

620

625

630

635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033

Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081

Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127

Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tggttaacaga agactgacaa gagtccttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttcctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttat 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaattggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag 2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1 5 10 15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20 25 30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35 40 45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100 105 110

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu

115 120 125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly

130 135 140



Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser  
145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr  
165 170 175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr  
180 185 190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu  
195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp  
210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala  
225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys  
245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu  
260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met  
275 280 285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(944)

<400> 126

tcaacgcctg cctccccctcg agcgtcctca gcgcagccgc cgcccgcgga gccagcacga 60

acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15

20

25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30

35

40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257

Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val

45

50

55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305

Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

60	65	70	75	
cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag	353			
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln				
80	85	90		
gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac	401			
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr				
95	100	105		
aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc	449			
Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg				
110	115	120		
aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt	497			
Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly				
125	130	135		
gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg	545			
Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu				
140	145	150	155	
gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac	593			
Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn				
160	165	170		
att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac	641			
Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn				
175	180	185		

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

210

215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833

Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881

Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984

Gly Leu Tyr Ala Met

285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttcct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcatcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acaccctaata gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatattt tgttggagcc actctgttcc tggctcagcc 1404

tcaaatagcag tatTTTTgtt gtgttctgtt gtttttatag cagggttggg gtggTTTTtg 1464

agccatgcgt gggTggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1

5

10

15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20

25

30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35

40

45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50

55

60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65

70

75

80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85

90

95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

100

105

110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

115

120

125

Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58

Met Ala Cys

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ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5

10

15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154

Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu

20

25

30

35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202

Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn

40

45

50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250

Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly

55

60

65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298

Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly

70

75

80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346

Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val

85

90

95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394

Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu

100

105

110

115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442

Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys

120

125

130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494

Val Ala Phe Asp

135

ctctgctccc ctg

507

<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

1

5

10

15



Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn

20

25

30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35

40

45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50

55

60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65

70

75

80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85

90

95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

100

105

110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

115

120

125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile

130

135

140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu

145

150

155

160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro

165

170

175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg

180

185

190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr

195

200

205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu

210

215

220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu

225

230

235

240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu

245

250

255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr

260

265

270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln

275

280

285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys

290

295

300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val

305

310

315

320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala  
325 330 335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe  
340 345 350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp  
355 360 365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln  
370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp  
385 390 395 400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu  
405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe  
420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn  
435 440 445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile  
450 455 460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp  
465 470 475 480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu

485

490

495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser

500

505

510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr

515

520

525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn

530

535

540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly

545

550

555

560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln

565

570

575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln

580

585

590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn

595

600

605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe

610

615

620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

625

630

635

640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

645

650

655

Leu Arg Ile Ser Glu Lys

660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(2059)

<400> 130

cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata 60

tcagtgggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

1

5

10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15

20

25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

30

35

40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

45

50

55

60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

65

70

75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349

Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

80

85

90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397

Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu

95

100

105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445

Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly

110

115

120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493

Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys

125

130

135

140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541

Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr  
 145 150 155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589  
 Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr  
 160 165 170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637  
 Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn  
 175 180 185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685  
 Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val  
 190 195 200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733  
 Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser  
 205 210 215 220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781  
 Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe  
 225 230 235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829  
 Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly  
 240 245 250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877  
 His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

255

260

265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925

Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu

270

275

280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973

Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp

285

290

295

300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021

Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp

305

310

315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069

Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln

320

325

330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117

Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile

335

340

345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165

Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr

350

355

360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213

Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr

365

370

375

380



aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261

Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg

385

390

395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309

Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu

400

405

410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357

Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415

420

425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405

Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

430

435

440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453

Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro

445

450

455

460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501

Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp

465

470

475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549

Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr

480

485

490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597

Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr

495

500

505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645

Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val

510

515

520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693

Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys

525

530

535

540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

575

580

585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885

His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590

595

600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933

Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr  
605 610 615 620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981  
Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe  
625 630 635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029  
Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser  
640 645 650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079  
Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys  
655 660

gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199

aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct 2251

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<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala

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15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg

20

25

30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala

35

40

45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg

50

55

60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys

65

70

75

80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met

85

90

95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala

100

105

110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys

115

120

125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val

130

135

140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp

145

150

155

160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile  
165 170 175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val  
180 185 190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val  
195 200 205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu  
210 215 220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro  
225 230 235 240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro  
245 250 255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys  
260 265 270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr  
275 280 285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val  
290 295 300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp  
305 310 315 320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp  
 325 330 335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn  
 340 345 350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu  
 355 360 365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu  
 370 375 380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu  
 385 390 395 400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly  
 405 410 415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn  
 420 425 430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu  
 435 440 445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys  
 450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu



Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp  
625 630 635 640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser  
645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu  
660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu  
675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu  
690 695 700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly  
705 710 715 720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro  
725 730 735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser  
740 745 750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro  
755 760 765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp  
770 775 780



Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg  
785 790 795 800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser  
805 810 815

Asp Arg Leu Arg Ile Ser Glu Lys  
820

<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (165)..(2636)

<400> 132

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ccccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggccgag gcccgtagcg 120

gggcgggcgg gagccccggc agtccggggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

5 10 15 20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25 30 35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc ccg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

40 45 50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55 60 65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

70 75 80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

85 90 95 100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512

Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr

105 110 115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560

Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn

120

125

130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608

Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys

135

140

145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656

Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn

150

155

160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704

Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val

165

170

175

180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc 752

His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe

185

190

195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca 800

Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro

200

205

210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848

Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln

215

220

225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896

Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

230

235

240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944

Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp

245

250

255

260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992

Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met

265

270

275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040

Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val

280

285

290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088

Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

295

300

305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136

Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn

310

315

320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184

Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala

325

330

335

340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232

Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His

345

350

355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280

Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu

360

365

370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328

Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu

375

380

385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag 1376

Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys

390

395

400

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt 1424

Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe

405

410

415

420

ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct 1472

Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser

425

430

435

gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa 1520

Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys

440

445

450

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat 1568

Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn

455

460

465

gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc 1616

Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala

470

475

480

aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664

Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu

485

490

495

500

atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712

Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys

505

510

515

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760

Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val

520

525

530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808

Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu

535

540

545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856

Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile

550

555

560

cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg 1904

Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp

565

570

575

580

gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt 1952

Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys  
585 590 595

ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg 2000  
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met  
600 605 610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt 2048  
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys  
615 620 625

gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa 2096  
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys  
630 635 640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca 2144  
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser  
645 650 655 660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa 2192  
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln  
665 670 675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240  
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr  
680 685 690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288  
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly

695

700

705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336

Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys

710

715

720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384

Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser

725

730

735

740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432

Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro

745

750

755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480

Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr

760

765

770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528

Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser

775

780

785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576

Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro

790

795

800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624

Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg

805

810

815

820



att tct gaa aaa tgacctcctt gtttttgaaa gtttagcataa ttttagatgc 2676

Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct 2828

<210> 133

<211> 919

<212> PRT

<213> Homo sapiens

<400> 133

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr

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Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser

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30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys

35

40

45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

50

55

60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys  
65 70 75 80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu  
85 90 95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile  
100 105 110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu  
115 120 125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu  
130 135 140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr  
145 150 155 160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe  
165 170 175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr  
180 185 190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly  
195 200 205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg  
210 215 220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu  
225 230 235 240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr  
245 250 255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr  
260 265 270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly  
275 280 285

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala  
290 295 300

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu  
305 310 315 320

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro  
325 330 335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr  
340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser  
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly

370

375

380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala

385

390

395

400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile

405

410

415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala

420

425

430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg

435

440

445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys

450

455

460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys

465

470

475

480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys

485

490

495

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln

500

505

510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala

515

520

525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile  
530 535 540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile  
545 550 555 560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr  
565 570 575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln  
580 585 590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser  
595 600 605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His  
610 615 620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala  
625 630 635 640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp  
645 650 655

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala  
660 665 670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala  
675 680 685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg  
690 695 700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala  
705 710 715 720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp  
725 730 735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu  
740 745 750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp  
755 760 765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile  
770 775 780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp  
785 790 795 800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val  
805 810 815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser  
820 825 830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

835

840

845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu

850

855

860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe

865

870

875

880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys

885

890

895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr

900

905

910

Ser Ser Ser Phe Leu Glu Val

915

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (427)..(3183)

<400> 134

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gagcaggctc ccgcctcgca ccgctgcccc gcgagcagct cctcttctcc cgaggcgcg 180

ggggcgcccc cgcgagcccc gcggctgaga ccccgagcc tggaggagg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtggga gcagccgtgg gacgcgtggc cgggagcggg 300

ggtgacagcc tgggattccg ggggcttctc ttcttctcc tctcctctc ctctctattc 360

ccagtgtggc cgtggctgac actaaagact ttgtagccat caacccgagt gcagtttcga 420

tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn

1 5 10

gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516

Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro

15 20 25 30

gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta 564

Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu

35 40 45

aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag 612

Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu

50 55 60



ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag 660

Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln

65

70

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ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt 708

Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser

80

85

90

gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata 756

Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile

95

100

105

110

ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804

Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys

115

120

125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852

Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

130

135

140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900

Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly

145

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155

gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948

Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

160

165

170

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt 996

Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly  
175 180 185 190

gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act 1044  
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr  
195 200 205

aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg 1092  
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu  
210 215 220

gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat 1140  
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn  
225 230 235

tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca 1188  
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro  
240 245 250

aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc 1236  
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser  
255 260 265 270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta 1284  
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu  
275 280 285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct 1332  
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala

290

295

300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380

Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu

305

310

315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428

Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys

320

325

330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat 1476

Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp

335

340

345

350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524

Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355

360

365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572

Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

370

375

380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620

Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn

385

390

395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668

Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala

400

405

410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716

Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu

415 420 425 430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764

Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr

435 440 445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812

Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala

450 455 460

gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt 1860

Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe

465 470 475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag 1908

Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln

480 485 490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956

Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr

495 500 505 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004

Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala

515 520 525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052  
 Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val  
 530 535 540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100  
 Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr  
 545 550 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148  
 Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln  
 560 565 570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196  
 Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr  
 575 580 585 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244  
 Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln  
 595 600 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292  
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 610 615 620

agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt 2340  
 Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val  
 625 630 635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct 2388

Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala  
640 645 650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa 2436  
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys  
655 660 665 670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg 2484  
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met  
675 680 685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc 2532  
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe  
690 695 700

gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca 2580  
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser  
705 710 715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att 2628  
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile  
720 725 730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga 2676  
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly  
735 740 745 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724  
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp

755

760

765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772

Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser

770

775

780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820

Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu

785

790

795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868

Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys

800

805

810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916

Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr

815

820

825

830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964

Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr

835

840

845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012

Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850

855

860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060

Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

865

870

875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108

Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880

885

890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156

Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895

900

905

910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203

Ser Thr Ser Ser Ser Phe Leu Glu Val

915

tatttgcaaa ctaggaattg cagtctgagg atcattttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

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aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaata 3503

cactatctat cttagataga tatatttttt tttattttta aatattgtac tatttatggt 3563

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<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln

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Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp

20 25 30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35 40 45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50 55 60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65 70 75 80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85 90 95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met

100 105 110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr

115 120 125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys  
130 135 140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe  
145 150 155 160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln  
165 170 175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala  
180 185 190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys  
195 200 205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile  
210 215 220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly  
225 230 235 240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser  
245 250 255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val  
260 265 270

Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu  
275 280 285

Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys

290

295

300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile

305

310

315

320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr

325

330

335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala

340

345

350

Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr

355

360

365

Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp

370

375

380

<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1589)

<400> 136

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cgggtcctca ggcggtgtt gctccggaac gggtggttgg ggaggggggg gtgggggggac 120

tctagacagc tgaggcgcga aagcgatgag tcctcggctc ttcctcctcc ttctccggga 180

cccgctctct gcctccctct ccaacgcccg gatgatctga gccgcgaggg cgccgacagc 240

cgggggcccc gacgcagccc ggctcctccc ctctccgcc ccttccccag cctgacctgg 300

cccgccgctg cagcggtgac ccctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360

tccccggctg ccgccgccgc cgcctcggcc gaccaggagc ctgcccgcct gcggctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473

Met Gly Ala Phe Leu Asp Lys Pro Lys Met

1 5 10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521

Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu

15 20 25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30 35 40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

50

55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60

65

70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75

80

85

90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95

100

105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn

140

145

150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953

Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu

155

160

165

170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001

Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg

175

180

185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049

Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr

190

195

200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097

Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu

205

210

215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145

Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile

220

225

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atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193

Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu

235

240

245

250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241

Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys

255

260

265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289

Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp

270

275

280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg 1337

Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser

285

290

295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385

Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys

300

305

310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433

Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu

315

320

325

330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481

Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro

335

340

345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529

Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350

355

360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577

Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

365

370

375

gat gat atg tgg taaaactgct catctagcca tggagtgttac cttcacctcc 1629

Asp Asp Met Trp

380

aaaggagagt acagctcaac ttgttgaaa cttttaacat ccacacctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaa at cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catattta at tatgaactgc tttaa atcac 1929

tatcaaagtt acaagaa atg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtc atggtt gtgtttggac ttgggggttg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaa atgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtaataa tacagtgtat tcataaga at ctcaatcttg gggctaa atg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatca at aaagcttgat ttaacaaaca agaaactt 2467

<210> 137



<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val

1 5 10 15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

20 25 30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35 40 45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50 55 60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

65 70 75 80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

85 90 95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser

100 105 110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser

115 120 125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met  
130 135 140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala  
145 150 155 160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser  
165 170 175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr  
180 185 190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln  
195 200 205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln  
210 215 220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro  
225 230 235 240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln  
245 250 255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln  
260 265 270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr  
275 280 285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln  
290 295 300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly  
305 310 315 320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro  
325 330 335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln  
340 345 350

Pro Gly Pro Gly Tyr Arg  
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<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

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Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

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10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

50

55

60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

65

70

75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

80

85

90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337

Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

95

100

105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385

Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala

110

115

120

125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433

Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

130

135

140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481

Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro

145

150

155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529

Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160

165

170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577

Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro

175

180

185

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac 625

Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr

190

195

200

205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673

Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln

210

215

220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721

Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln

225

230

235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769

Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro

240

245

250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817

Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu

255

260

265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865

Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln

270

275

280

285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913

Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro

290

295

300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961

Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro

305

310

315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009

Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro

320

325

330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057

Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly

335

340

345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104

Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350

355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag cattttttat gatattcattg ttggtgttaa 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga 1344

cttgactttc tagcttcctt tgtccggagg atattaaaat gctaggggtga gggttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc 1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1

5

10

15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

20

25

30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35

40

45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50

55

60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65

70

75

80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85

90

95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu

100

105

110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu

115

120

125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg

130

135

140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val

145

150

155

160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu

165

170

175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val



180

185

190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp

195

200

205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro

210

215

220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr

225

230

235

240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala

245

250

255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr

260

265

270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly

275

280

285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro

290

295

300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr

305

310

315

320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr

325

330

335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala  
 340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr  
 355 360 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe  
 370 375 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg  
 385 390 395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta 51

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu

1

5

10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99

Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

15

20

25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147

Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

30

35

40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195

Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

45

50

55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

60

65

70

75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80

85

90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95

100

105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387

Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu

110

115

120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435

Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp

125

130

135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483

Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys

140

145

150

155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531

Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu

160

165

170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579

Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu

175

180

185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627

Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

190

195

200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675

Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro

205

210

215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723

Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln

220

225

230

235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771

Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala

240

245

250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819  
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln  
255 260 265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867  
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln  
270 275 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915  
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala  
285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963  
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr  
300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011  
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln  
320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059  
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro  
335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107  
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro  
350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155

Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg  
 365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203  
 Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr  
 380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256  
 Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gatattcattg ttgggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttacttttga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg 1496

atattaaaat gctaggggtga ggttttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly

85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val

100 105 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe

115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr

130 135 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile  
145 150 155 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe  
165 170 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro  
180 185 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser  
195 200 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile  
210 215 220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe  
225 230 235 240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly  
245 250 255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln  
260 265 270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala  
275 280 285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu  
290 295 300



Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His  
305 310 315 320

Val Gln Thr

<210> 142  
<211> 1616  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (72)..(1040)

<400> 142

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gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

1 5 10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158

Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu

15 20 25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206

Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe  
30 35 40 45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254  
Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His  
50 55 60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302  
Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg  
65 70 75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350  
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe  
80 85 90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398  
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp  
95 100 105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446  
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg  
110 115 120 125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494  
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln  
130 135 140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542  
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

145

150

155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590

Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly

160

165

170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638

Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

175

180

185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686

Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190

195

200

205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734

Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

210

215

220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782

Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

225

230

235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830

Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn

240

245

250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878

Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val

255

260

265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926  
 Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu  
 270 275 280 285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974  
 Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu  
 290 295 300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022  
 Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln  
 305 310 315

ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg 1070  
 Leu Thr His Val Gln Thr  
 320

ctggggtgtg gggcagtctg ggtcctctca tcattccccac ttcccaggcc cagcctttcc 1130

aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tcctgcttct 1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250

cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtccccctcc catccccccac 1370

gcagctccac cccagtccca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430

agccccctcct ctctgacctt taacctcact ctcaccttgc accgtgcacc aacccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85

90

95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His

100

105

110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe

115

120

125

Leu Gln Pro Leu Met His Cys Val

130

135

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(632)

<400> 144

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ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572

Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser

105

110

115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620

Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu

120

125

130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672

Met His Cys Val

135

ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaaccctc atgtgggggt 732

ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792

atttttcctg ttttaaattc taggatagat tttaacatcc ttgcggtcc cagtccaagg 852

taggctgggtg tcatagtctt ctcactccta atccatgacc actgtttttt tcctatttat 912

atcaccaggt agcctactga gttaatattt aagtgtgcaa tagataagtg tccctgtttt 972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaa at ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212



gtgtagatcc aatcacttaa ataaacctgt atgtatatgc

1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1

5

10

15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe

20

25

30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln

35

40

45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg

50

55

60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro

65

70

75

80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu

85

90

95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser

100	105	110
Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu		
115	120	125
Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu		
130	135	140
Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met		
145	150	155 160
Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp		
165	170	175
Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val		
180	185	190
Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu		
195	200	205
Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp		
210	215	220
Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile		
225	230	235 240
Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala		
245	250	255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu  
260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe  
275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe  
290 295 300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys  
305 310 315 320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser  
325 330 335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile  
340 345 350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met  
355 360 365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys  
370 375 380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile  
385 390 395 400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala  
405 410 415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

440

445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

460

Ala Ser Gly Ile

465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379)..(1782)

<400> 146

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatcgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1

5

10

tgc tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459

Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15

20

25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507

Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

30

35

40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45

50

55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603

Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala

60

65

70

75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

80

85

90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699

Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe

95

100

105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747

Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg

110

115

120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125

130

135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys

140

145

150

155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile

160

165

170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939

Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val

175

180

185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987

Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile

190

195

200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035

Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met

205

210

215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083

Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu

220

225

230

235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131

Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu

240

245

250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179

Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val

255

260

265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227

Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln

270

275

280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu

285

290

295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323

Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr

300

305

310

315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt 1371  
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser  
320 325 330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac 1419  
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His  
335 340 345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg 1467  
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu  
350 355 360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515  
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr  
365 370 375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563  
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala  
380 385 390 395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611  
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu  
400 405 410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659  
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser  
415 420 425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707



Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe  
 430 435 440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755  
 Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe  
 445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802  
 Ile Asn Asp Asn Ala Ala Ser Gly Ile  
 460 465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaata ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

- <210> 147
- <211> 460
- <212> PRT
- <213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp  
 1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly  
 20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro

35

40

45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr

50

55

60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr

65

70

75

80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val

85

90

95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu

100

105

110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile

115

120

125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly

130

135

140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile

145

150

155

160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg

165

170

175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met

180	185	190
Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp		
195	200	205
Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala		
210	215	220
Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp		
225	230	235 240
Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro		
245	250	255
Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg		
260	265	270
Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile		
275	280	285
Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu		
290	295	300
Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg		
305	310	315 320
Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg		
325	330	335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu  
340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser  
355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val  
370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val  
385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu  
405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys  
420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys  
435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile  
450 455 460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376)..(1755)

<400> 148

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gccttccgtc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180

acatttatTT caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15

20

25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30

35

40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45 50 55 60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65 70 75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80 85 90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699

Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95 100 105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747

Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile

110 115 120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795

Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His

125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843

Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu

145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891  
 Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr  
 160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939  
 Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu  
 175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987  
 Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile  
 190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035  
 Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly  
 205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083  
 Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu  
 225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131  
 His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys  
 240 245 250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179  
 Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp  
 255 260 265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227

Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp  
270 275 280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275  
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala  
285 290 295 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323  
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe  
305 310 315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371  
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met  
320 325 330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419  
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys  
335 340 345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467  
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe  
350 355 360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515  
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile  
365 370 375 380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563  
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp



385

390

395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611

Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys

400

405

410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659

Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser

415

420

425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707

Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe

430

435

440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755

Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

445

450

455

460

tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaatt 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc 1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser

130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
145 150 155 160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
165 170 175

Asp Arg His Lys Met Leu Ser  
180

<210> 150  
<211> 1562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (120)..(668)

<400> 150

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ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
1 5 10 15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

25

30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65

70

75

80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85

90

95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100

105

110

gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser

130

135

140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698

Asp Arg His Lys Met Leu Ser

180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctccttccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctccttctcc ctaacttttag 818

aaatgttgta cttggctatt ttgattaggg aagagggatg tggtctctga tctccgttgt 878

cttcttgggt ctttgggggt gaaggagggg ggaaggcagg ccagaaggga atggagacat 938

tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 998

cagctctgag tcttgggaat gttgttacc ttggaagata aagctgggtc ttcaggaact 1058

cagtgtctgg gaggaaagca tggcccagca ttcagcatgt gttcctttct gcagtgggtc 1118

tttatcacca ctccttccc agccccagcg cctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctgggcccc tgagcccact gggctctcag ggtgcactgg 1238

aagctgggtgt tcgctgtccc ctgtgcactt ctgcactgg ggcatggagt gcccatgcat 1298

actctgctgc cggccccctc acctgcactt gaggggtctg ggcagtcct cctctcccca 1358

gtgtccacag tcactgagcc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagcccct gtacttgggt tgcctcttgt ccctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc 1562

<210> 151

<211> 2815

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)..(2387)

<400> 151

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cagccaggtc tgtgctgccg ccctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180

ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly

1

5

10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278

Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys

15

20

25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326

Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala

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40

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atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374

Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu

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gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422

Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp

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gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470

Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser

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tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518

Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys

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ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566

Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe

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gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614

Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp

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gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662

Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro

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ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710

Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala

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gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758

Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp

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gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806

Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His

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cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat 854

Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His

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gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag 902

Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln

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gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc 950

Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser

240

245

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tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa 998

Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu

255

260

265

att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct 1046

Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro

270

275

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gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc 1094

Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys

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aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa 1142

Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu

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agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt 1190

Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val

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cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct 1238

Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro

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gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct 1286

Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro

350

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360

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ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc 1334

Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser

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aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat 1382

Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr

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aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt 1430

Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg

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att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc 1478

Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe

415

420

425

tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa 1526

Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln

430

435

440

445

gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc 1574

Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser  
 450 455 460

ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac 1622  
 Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn  
 465 470 475

agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca 1670  
 Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro  
 480 485 490

ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc 1718  
 Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu  
 495 500 505

cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag 1766  
 His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys  
 510 515 520 525

gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc 1814  
 Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg  
 530 535 540

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag 1862  
 Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln  
 545 550 555

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca 1910  
 Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr

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Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu

575

580

585

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc 2006

Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser

590

595

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tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act 2054

Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr

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615

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cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca 2102

Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro

625

630

635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg 2150

Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu

640

645

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cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc 2198

Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser

655

660

665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246

Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala

670

675

680

685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294

Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly

690

695

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gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg 2342

Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met

705

710

715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387

Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

720

725

730

tgaccaggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507

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accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg 2627

actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687

gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggtctct 2747

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20 25 30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu  
35 40 45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu  
50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met  
65 70 75 80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val  
85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser  
100 105 110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln

115	120	125
Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys		
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Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser		
145	150	155 160
His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg		
165	170	175
Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr		
180	185	190
Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile		
195	200	205
Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His		
210	215	220
Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln		
225	230	235 240
Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro		
245	250	255
Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val		
260	265	270

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu  
275 280 285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu  
290 295 300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly  
305 310 315 320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly  
325 330 335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro  
340 345 350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser  
355 360 365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro  
370 375 380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val  
385 390 395 400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu  
405 410 415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu  
420 425 430



Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile

435

440

445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys

450

455

460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr

465

470

475

480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys

485

490

495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile

500

505

510

Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn

515

520

525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys

530

535

540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala

545

550

555

560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val

565

570

575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala

580

585

590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly

595

600

605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe

610

615

620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro

625

630

635

640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val

645

650

655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro

660

665

670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val

675

680

685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser

690

695

700

Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu

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710

715

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Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

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Met Ala Cys Thr Gly Pro

1

5

tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162

Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys

10

15

20

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210

Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln

25

30

35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258

Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu

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45

50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306  
 Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala  
 55 60 65 70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354  
 Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro  
 75 80 85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402  
 Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu  
 90 95 100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450  
 Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr  
 105 110 115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498  
 Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly  
 120 125 130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg 546  
 Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly  
 135 140 145 150

gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca 594  
 Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro  
 155 160 165

cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att 642

Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile

170

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Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly

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agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc 738

Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr

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atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc 786

Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu

215

220

225

230

tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc 834

Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly

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240

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tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc 882

Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala

250

255

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agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg 930

Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val

265

270

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gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca 978

Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro  
280 285 290

gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc 1026  
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly  
295 300 305 310

ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc 1074  
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys  
315 320 325

tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc 1122  
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr  
330 335 340

tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca 1170  
Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr  
345 350 355

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cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg 1266  
His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser  
375 380 385 390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa 1314  
Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu

395

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cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc 1362

His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro

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gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag 1410

Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu

425

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ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta 1458

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ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac 1506

Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn

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caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc 1554

Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val

475

480

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atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac 1602

Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp

490

495

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acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag 1650

Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln

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510

515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag 1698

Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln

520

525

530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg 1746

Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg

535

540

545

550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg 1794

Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu

555

560

565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca 1842

Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala

570

575

580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg 1890

Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly

585

590

595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938

Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro

600

605

610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986

Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro

615

620

625

630



cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034

Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro

635

640

645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082

Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala

650

655

660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130

Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro

665

670

675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178

Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His

680

685

690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226

Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu

695

700

705

710

gca gaa tgaccgcgtg tccttgccctg accacctggg gaacaccctt ggaccaggc 2282

Ala Glu

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gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc 2402

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2544

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Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr

20

25

30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu

35

40

45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu

50

55

60

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val

65

70

75

80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val

85

90

95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser  
100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg  
115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys  
130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser  
145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg  
165 170 175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys  
180 185 190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu  
195 200 205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro  
210 215 220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro  
225 230 235 240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro  
245 250 255

Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro  
260 265 270

Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro  
275 280 285

Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys  
290 295 300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu  
305 310 315 320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu  
325 330 335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr  
340 345 350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser  
355 360 365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser  
370 375 380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu  
385 390 395 400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu

405

410

415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln

420

425

430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His

435

440

445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu

450

455

460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln

465

470

475

480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro

485

490

495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg

500

505

510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe

515

520

525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln

530

535

540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg

545

550

555

560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser  
565 570 575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly  
580 585 590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro  
595 600 605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp  
610 615 620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr  
625 630 635 640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro  
645 650 655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln  
660 665 670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln  
675 680 685

Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro  
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Glu Asp Lys Thr Gln Glu Ala Glu  
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ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca 295

Met Lys Lys Lys Ser

1

5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343

Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu

10

15

20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc 391

Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu

25

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35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439

Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala

40

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cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487

Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp

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tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535

Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro

70

75

80

85

ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac 583

Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp

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atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631

Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly

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gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679

Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser

120

125

130

ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727



Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys  
135 140 145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775  
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser  
150 155 160 165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc 823  
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly  
170 175 180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggc 871  
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly  
185 190 195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag 919  
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu  
200 205 210

gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc 967  
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu  
215 220 225

att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag 1015  
Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu  
230 235 240 245

gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg 1063  
Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu

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255

260

cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag 1111

Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu

265

270

275

tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc 1159

Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile

280

285

290

ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg 1207

Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala

295

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ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg 1255

Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly

310

315

320

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gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac 1303

Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr

330

335

340

atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc 1351

Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly

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350

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ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag 1399

Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu

360

365

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aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa 1447

Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys

375

380

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ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg 1495

Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu

390

395

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agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc 1543

Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile

410

415

420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag 1591

Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln

425

430

435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc 1639

Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala

440

445

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tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag 1687

Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys

455

460

465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg 1735

Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro

470

475

480

485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag 1783  
 Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu  
 490 495 500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg 1831  
 Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu  
 505 510 515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc 1879  
 Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile  
 520 525 530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac 1927  
 Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp  
 535 540 545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta 1975  
 Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val  
 550 555 560 565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg 2023  
 Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp  
 570 575 580

gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca 2071  
 Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala  
 585 590 595

cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag 2119

Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu  
600 605 610

gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa 2167  
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu  
615 620 625

ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg 2215  
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg  
630 635 640 645

aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc 2263  
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser  
650 655 660

acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc 2311  
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser  
665 670 675

tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc 2359  
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr  
680 685 690

tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg 2407  
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu  
695 700 705

ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac 2455  
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr

710	715	720	725	
ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca				2503
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro				
	730	735	740	
atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc				2551
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser				
	745	750	755	
cct cca ccc tgc ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg				2599
Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu				
	760	765	770	
agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc				2647
Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu				
	775	780	785	
cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc				2695
Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser				
790	795	800	805	
cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg				2743
Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg				
	810	815	820	
act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg				2791
Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly				
	825	830	835	

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg 2839

Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly

840

845

850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg 2887

Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly

855

860

865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag 2935

Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln

870

875

880

885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983

His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu

890

895

900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gagggcccca 3036

Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

905

910

agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc 3096

ttcagctact gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc 3156

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ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagg tcagctcgag 3276

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gattcactcc tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg 3396

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<210> 156

<211> 912

<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg

1

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Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn

20

25

30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr

35

40

45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu

50

55

60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro

65

70

75

80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg



85

90

95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met

100

105

110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr

115

120

125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr

130

135

140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe

145

150

155

160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met

165

170

175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro

180

185

190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu

195

200

205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp

210

215

220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln

225

230

235

240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser  
245 250 255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu  
260 265 270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg  
275 280 285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp  
290 295 300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala  
305 310 315 320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser  
325 330 335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met  
340 345 350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr  
355 360 365

Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser  
370 375 380

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu  
385 390 395 400

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala  
405 410 415

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn  
420 425 430

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val  
435 440 445

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val  
450 455 460

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile  
465 470 475 480

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser  
485 490 495

Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe  
500 505 510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu  
515 520 525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys  
530 535 540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu

545	550	555	560
Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala			
	565	570	575
Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu			
	580	585	590
Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln			
	595	600	605
Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu			
	610	615	620
Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser			
625	630	635	640
Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys			
	645	650	655
Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro			
	660	665	670
Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser			
	675	680	685
Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro			
690	695	700	

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser  
705 710 715 720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe  
725 730 735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser  
740 745 750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr  
755 760 765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser  
770 775 780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr  
785 790 795 800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro  
805 810 815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser  
820 825 830

Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val  
835 840 845

Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly  
850 855 860

Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro  
865 870 875 880

Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg  
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Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val  
900 905 910

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<400> 157

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cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172

Met His Tyr Asp Gly His Val

1 5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220

Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser

10

15

20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag 268

Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu

25

30

35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca 316

Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr

40

45

50

55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac 364

Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp

60

65

70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att 412

Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile

75

80

85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg 460

Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val

90

95

100

ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac 508

Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp

105

110

115

atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc 556  
 Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala  
 120 125 130 135

tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct 604  
 Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro  
 140 145 150

gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg 652  
 Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu  
 155 160 165

agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag 700  
 Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu  
 170 175 180

cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct 748  
 Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro  
 185 190 195

ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc 796  
 Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile  
 200 205 210 215

ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc 844  
 Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly  
 220 225 230

agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc 892



Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala  
 235 240 245

agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt 940  
 Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe  
 250 255 260

ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc 988  
 Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr  
 265 270 275

tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac 1036  
 Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp  
 280 285 290 295

cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat 1084  
 His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn  
 300 305 310

gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat 1132  
 Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His  
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gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag 1180  
 Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu  
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ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc 1228  
 Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile

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aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg 1276

Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu

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Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala

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cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag 1372

Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu

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aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa 1420

Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys

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Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys

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Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp

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Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg

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Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu

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Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu

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cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg 1756

Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg

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Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val

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gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac 1852

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Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr  
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aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg 2044  
Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu  
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Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile  
665 670 675

tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca 2236  
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Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln  
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gag gag gaa gag gag gag gag gag gag gag gag gaa ggc gag gac agt 2332  
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ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc 2380  
 Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly  
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act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg 2572  
 Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro  
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gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc 2620  
 Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser

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cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta 2668

Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu

825

830

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gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg 2716

Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser

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845

850

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ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc 2764

Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro

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cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca 2812

His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala

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ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca 2860

Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser

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Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser

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cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct 2956

Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro

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Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu

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Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser

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Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly

35

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Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala

50

55

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Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys

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70

75

80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys



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Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly

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105

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Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro

115

120

125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg

130

135

140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly

145

150

155

160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly

165

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Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu

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Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu

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Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser

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Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp

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Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser  
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Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln  
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Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu  
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Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp  
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Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp  
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Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His  
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Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile  
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Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn  
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Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe  
370 375 380

Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser  
385 390 395 400

Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu  
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Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe  
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Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr  
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Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr  
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Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met  
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Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys  
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Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val  
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Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys  
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Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg

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Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe

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Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr

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615

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Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu

625

630

635

640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His

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650

655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys

660

665

670

Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln

675

680

685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu

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695

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Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu  
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Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr  
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Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser  
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Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp  
755 760 765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser  
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785 790 795 800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp  
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Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala  
820 825 830

Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg  
835 840 845

Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val  
850 855 860

Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala  
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Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser  
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Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro  
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Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp  
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Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys  
930 935 940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu  
945 950 955 960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val  
965 970 975

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Met Gly Trp Lys Pro Ser Glu

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Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

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Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu

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Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys

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gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545

Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

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gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593

Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

155 160 165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641



His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg  
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Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg  
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Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp  
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cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977  
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser

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Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu

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gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073

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ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121

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aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag 1505

Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys

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agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553

Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475

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Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val

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Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu

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555 560 565

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Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu  
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Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln  
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Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys  
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ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273  
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu  
715 720 725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321  
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu  
730 735 740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369  
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu

745

750

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ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417

Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu

760

765

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Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr

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gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513

Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val

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agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561

Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu

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ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609

Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu

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cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657

Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly

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acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705

Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro

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gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753

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Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg

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atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849

Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg

905

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cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897

Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro

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cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945

Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu

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945

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cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc 2993

Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe

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965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041

Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

970

975

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tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089

Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

35

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Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp

50

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60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val

65

70

75

80



Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val  
85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr  
100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val  
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg  
130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr  
145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg  
165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly  
180 185 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val  
195 200 205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys  
210 215 220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg

225	230	235	240
Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg			
	245	250	255
Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala			
	260	265	270
Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala			
	275	280	285
Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly			
	290	295	300
Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln			
305	310	315	320
Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln			
	325	330	335
Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln			
	340	345	350
Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys			
	355	360	365
His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu			
	370	375	380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp  
385 390 395 400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly  
405 410 415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser  
420 425 430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp  
435 440 445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu  
450 455 460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu  
465 470 475 480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu  
485 490 495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala  
500 505 510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu  
515 520 525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr  
530 535 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val  
545 550 555 560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser  
565 570 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg  
580 585 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser  
595 600 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly  
610 615 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr  
625 630 635 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His  
645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp  
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn  
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp

690

695

700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val

705

710

715

720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys

725

730

735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala

740

745

750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly

755

760

765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu

770

775

780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu

785

790

795

800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser

805

810

815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly

820

825

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Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

835

840

845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His  
850 855 860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser  
865 870 875 880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val  
885 890 895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val  
900 905 910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala  
915 920 925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser  
930 935 940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp  
945 950 955 960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro  
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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag 113

Met Gly Trp Lys Pro Ser Glu

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gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

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agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209

Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg

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gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257

Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val

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Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp

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ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353

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Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly

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acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449

Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu

105

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ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497

Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys

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gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545

Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

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Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

155

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cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641

His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg

170

175

180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689

Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg

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Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp

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Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile

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cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833

Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp

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gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881

Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val

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255

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gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929

Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp

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cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977  
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser  
280 285 290 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025  
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu  
300 305 310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073  
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn  
315 320 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121  
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gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag 1265  
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Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg  
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 Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala  
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 Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly  
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 Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val  
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ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg 1697

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Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu

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ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg 1793

Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg

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gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841

Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val

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cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889

Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys

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gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937

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atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag 1985

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ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081

Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile

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ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129

Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe

665

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acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag 2177

Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln

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atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag 2225

Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys

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ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273

Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu

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gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321

Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu

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gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369  
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ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417  
 Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu  
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ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465  
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gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513  
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agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561  
 Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu  
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ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609  
 Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu  
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cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657  
 Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly  
 840 845 850 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705

Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro  
860 865 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753  
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu  
875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801  
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg  
890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849  
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg  
905 910 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897  
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920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945  
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu  
940 945 950

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc 2993  
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe  
955 960 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041  
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

970

975

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tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089

Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

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3168

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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

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Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp

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55

60



Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val  
65 70 75 80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val  
85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr  
100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val  
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg  
130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr  
145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg  
165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly  
180 185 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val  
195 200 205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys  
210 215 220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg  
225 230 235 240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg  
245 250 255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala  
260 265 270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala  
275 280 285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly  
290 295 300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln  
305 310 315 320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln  
325 330 335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln  
340 345 350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys  
355 360 365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu

370

375

380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp

385

390

395

400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly

405

410

415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser

420

425

430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp

435

440

445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu

450

455

460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu

465

470

475

480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu

485

490

495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala

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505

510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu

515

520

525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr  
530 535 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val  
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Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser  
565 570 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg  
580 585 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser  
595 600 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly  
610 615 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr  
625 630 635 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His  
645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp  
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn  
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp  
690 695 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val  
705 710 715 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys  
725 730 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala  
740 745 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly  
755 760 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu  
770 775 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu  
785 790 795 800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser  
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly  
820 825 830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

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845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His

850

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860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser

865

870

875

880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val

885

890

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Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val

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Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala

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Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser

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Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp

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Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

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Met Ile Ala Trp Arg Leu Pro Leu

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Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly

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Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala

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gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258

Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr

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Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu

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Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu

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gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402

Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln

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Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro

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Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr

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Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp

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Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala  
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gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg 642  
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser  
170 175 180

gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc 690  
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile  
185 190 195 200

tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta 738  
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205 210 215

gcc ttc att ggc atg tac cag acg atg act aag aag gca gcc atc act 786  
Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr  
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Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro  
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Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu

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tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg				978
Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly				
	285	290	295	
atg ctc ttt tgc ctg ggc ata ttc ttg tcc ttc tac ctg ctg act gtg				1026
Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val				
	300	305	310	
ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg				1074
Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu				
	315	320	325	
gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg				1122
Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu				
	330	335	340	
gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc				1170
Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly				
345	350	355	360	
tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca				1218
Ser Phe Glu Asn Gly Ser Gly Ser Thr Asp Gly Leu Val Glu Ser Ala				
	365	370	375	
ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag				1266
Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys				
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Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp

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Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser

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415

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Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp

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cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg 1506

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Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu

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Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile

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tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc 1650  
Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala  
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ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc 1698  
Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu  
525 530 535

ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg 1746  
Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu  
540 545 550

ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt 1794  
Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe  
555 560 565

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Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala  
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tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag 2130  
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ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac 2178  
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp  
685 690 695

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Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu  
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tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg 2370

Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg

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750

755

760

agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc 2418

Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr

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tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc 2466

Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser

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Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys

795

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Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser

810

815

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Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp

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Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe

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Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val

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Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

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Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

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Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro

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Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val

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Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln

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Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr

130

135

140

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu

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155

160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr

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170

175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys  
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro  
195 200 205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr  
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser  
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys  
245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp  
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val  
275 280 285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe  
290 295 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp  
305 310 315 320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro  
325 330 335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala  
340 345 350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser  
355 360 365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser  
370 375 380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met  
385 390 395 400

Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro  
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Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp  
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Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln  
435 440 445

Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg  
450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe  
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Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

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His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu

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Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg

530

535

540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu

545

550

555

560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr

565

570

575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro

580

585

590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala

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Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn

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620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe

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635

640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile  
645 650 655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln  
660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg  
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro  
690 695 700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn  
705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala  
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala  
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile  
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu  
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu  
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp

805

810

815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe

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845

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Met Phe Ala Leu Gly Leu Pro Phe Leu Val

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 Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu  
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 Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr  
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 Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys  
 60 65 70

cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg 353  
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 75 80 85 90

gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag 401  
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys  
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tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag 449  
 Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys  
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Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser

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cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt 545

Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe

140

145

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Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln

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170

ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att 641

Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile

175

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gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att 689

Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile

190

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cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc 737

Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe

205

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atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag 785

Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln

220

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230



cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag 833  
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acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca 881  
 Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala  
 255 260 265

gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg 929  
 Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val  
 270 275 280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc 977  
 Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu  
 285 290 295

ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg 1025  
 Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu  
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gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc 1073  
 Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala  
 315 320 325 330

att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat 1121  
 Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp  
 335 340 345

tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt 1169

Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe  
 350 355 360

gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act 1217  
 Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr  
 365 370 375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc 1265  
 Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg  
 380 385 390

ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc 1313  
 Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser  
 395 400 405 410

ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg 1361  
 Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val  
 415 420 425

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat 1409  
 Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn  
 430 435 440

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag 1457  
 Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys  
 445 450 455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att 1505  
 Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile

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gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc 1553

Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile

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acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac 1601

Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr

495

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tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac 1649

Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn

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aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg 1697

Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu

525

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ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc 1745

Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg

540

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aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt 1793

Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu

555

560

565

570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct 1841

Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala

575

580

585

tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg 1889

Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser

590

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ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag 1937

Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys

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610

615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg 1985

Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu

620

625

630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg 2033

Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly

635

640

645

650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc 2081

Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr

655

660

665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac 2129

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp

670

675

680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc 2177

Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile

685

690

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cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc 2225  
 Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val  
 700 705 710

atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg 2273  
 Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met  
 715 720 725 730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321  
 Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn  
 735 740 745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369  
 Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly  
 750 755 760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417  
 Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val  
 765 770 775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465  
 Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp  
 780 785 790

cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc 2513  
 Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu  
 795 800 805 810

ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc 2561

Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile  
815 820 825

gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg 2609  
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly  
830 835 840

tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg 2658  
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly  
845 850 855

tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca 2718

ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggaccaggg 2778

ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgtagtcat gcacacacat 2838

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tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc 3078

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<212> PRT

<213> Homo sapiens

<400> 166

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20 25 30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val  
35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly  
50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu  
65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro  
85 90 95

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val  
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln  
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr  
130 135 140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu  
145 150 155 160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr  
165 170 175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn  
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro  
195 200 205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr  
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser  
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys  
245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp  
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val  
275 280 285



Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe  
290 295 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp  
305 310 315 320

Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro  
325 330 335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser  
340 345 350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser  
355 360 365

Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly  
370 375 380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met  
385 390 395 400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr  
405 410 415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp  
420 425 430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln

435

440

445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg

450

455

460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe

465

470

475

480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

485

490

495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala

500

505

510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu

515

520

525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg

530

535

540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu

545

550

555

560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr

565

570

575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro

580

585

590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala  
595 600 605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn  
610 615 620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe  
625 630 635 640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile  
645 650 655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln  
660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg  
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro  
690 695 700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn  
705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala  
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala  
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile  
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu  
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu  
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp  
805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe  
820 825 830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser  
835 840 845

Ser Cys Leu Leu Pro Cys Gly  
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agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg 106

Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu

5

10

15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154

Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr

20

25

30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202

Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg

35

40

45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250

Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe

50

55

60

65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298

Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile

70

75

80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346  
 Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn  
 85 90 95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394  
 Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln  
 100 105 110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442  
 Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro  
 115 120 125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490  
 Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro  
 130 135 140 145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538  
 Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro  
 150 155 160

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591  
 Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys  
 165 170

agaggaggga caggagaggg cctttccctg gcctttctgt cttegttgat gttcacttcc 651

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gggc 2815

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<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

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Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu

20 25 30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser

35 40 45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp  
50 55 60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe  
65 70 75 80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe  
85 90 95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln  
100 105 110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn  
115 120 125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser  
130 135 140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr  
145 150 155 160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys  
165 170

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<213> Homo sapiens

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<222> (136)..(1755)

<400> 169

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agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile

1

5

10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219

Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu

15

20

25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267

Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala

30

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acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315

Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn

45

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55

60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363

Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu

65

70

75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411

Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr

80

85

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cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459

Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu

95

100

105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507

Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala

110

115

120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555

Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr

125

130

135

140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603

Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn

145

150

155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat 651

Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn

160

165

170

cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc 699

Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser

175

180

185

cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt 747

Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser

190

195

200

acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggc cct 795

Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro

205

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215

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gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg 843

Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg

225

230

235

gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc 891

Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr

240

245

250

tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag 939

Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu

255

260

265

ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc 987

Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser

270

275

280

agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc 1035

Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr

285

290

295

300

acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca 1083

Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro

305 310 315

gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc 1131

Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro

320 325 330

cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa 1179

Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys

335 340 345

ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct 1227

Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro

350 355 360

act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac 1275

Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp

365 370 375 380

ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc 1323

Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly

385 390 395

gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg 1371

Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg

400 405 410

ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419

Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val  
415 420 425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467  
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser  
430 435 440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat 1515  
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr  
445 450 455 460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563  
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile  
465 470 475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611  
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly  
480 485 490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659  
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys  
495 500 505

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg 1707  
His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly  
510 515 520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1755  
Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

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tgggttcttt tcagggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955

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ccgtcagcct ccagggatct acaccctgcc ttggctgcta cagctttttc actccactgc 3075

cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135

caagtccagc aacctgcacc ctggaaccag gagtggaccc taccgggct gtctgtatta 3195

atccccatcc cccaccacca atcttaaaaa gccctctgtc ccctaccct aaaccccagt 3255

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Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro

20

25

30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu

35

40

45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg

50

55

60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

65

70

75

80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln

85

90

95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu

100

105

110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile

115

120

125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val  
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala  
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly  
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser  
180 185 190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala  
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser  
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu  
225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser  
245 250 255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly  
260 265 270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu  
275 280 285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro  
290 295 300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser  
305 310 315 320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val  
325 330 335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn  
340 345 350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val  
355 360 365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg  
370 375 380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly  
385 390 395 400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser  
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe  
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly

435

440

445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly

450

455

460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu

465

470

475

480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln

485

490

495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser

500

505

510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val

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Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

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gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccg 180

gggaaggagg cagggaagg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1

5

10

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gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20

25

30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35

40

45

ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc 433

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

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aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc 481

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

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70

75

80

atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac 529

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp

85

90

95

ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga 577

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly

100

105

110

gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag 625

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys

115

120

125

cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg 673

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu

130

135

140

gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc 721

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser

145

150

155

160

gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg 769

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu

165

170

175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg 817

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

180

185

190

ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc 865

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser

195

200

205

cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc 913

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

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215

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agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca 961

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225

230

235

240

ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct 1009

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro

245

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255

ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc 1057

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu

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265

270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc 1105

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275

280

285

gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag 1153

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu

290

295

300



ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca 1201

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro

305 310 315 320

gac cca ccg tca cca ccg tcg cag cct ccg acc ccc gct acg gcg ccc 1249

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro

325 330 335

tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg 1297

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu

340 345 350

gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc 1345

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

355 360 365

aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa 1393

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln

370 375 380

tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc 1441

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val

385 390 395 400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag 1489

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu

405 410 415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc 1537

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala

420

425

430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag 1585

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu

435

440

445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa 1633

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys

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455

460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa 1681

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys

465

470

475

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gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc 1729

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe

485

490

495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag 1777

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys

500

505

510

cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag 1825

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515

520

525

gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac 1873

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

530

535

540

atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg 1921

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

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550

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gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat 1969

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr

565

570

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ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac 2017

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn

580

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cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag 2065

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

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ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag 2113

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys

610

615

620

caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa 2161

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln

625

630

635

640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac 2209

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp

645

650

655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga 2257

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly

660

665

670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat 2305

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr

675

680

685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac 2353

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn

690

695

700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc 2401

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg

705

710

715

720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc 2449

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe

725

730

735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg 2497

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly

740

745

750

aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg 2545

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg

755

760

765

gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg 2593  
 Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu  
 770 775 780

gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag 2641  
 Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu  
 785 790 795 800

acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg 2689  
 Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val  
 805 810 815

ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc 2737  
 Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala  
 820 825 830

cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc 2785  
 Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu  
 835 840 845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc 2833  
 Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala  
 850 855 860

ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac 2881  
 Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr  
 865 870 875 880

cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag 2929

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln  
885 890 895

ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag 2977  
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln  
900 905 910

ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc 3025  
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser  
915 920 925

agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt 3073  
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser  
930 935 940

gag ctg cag cgg ctc cgc agg tgaggagccc atggggcgagg cagccccag 3124  
Glu Leu Gln Arg Leu Arg Arg  
945 950

aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184

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ccagcacatg gaataaaata gccagggcca cactc 3579

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<212> PRT

<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

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Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

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Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35 40 45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

50 55 60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

65 70 75 80

Met Arg Asp Pro Asp Glu Asp Glu Glu Gly Thr Asp Glu Asp Asp

85

90

95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly

100

105

110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys

115

120

125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu

130

135

140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser

145

150

155

160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu

165

170

175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

180

185

190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser

195

200

205

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

210

215

220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225

230

235

240



Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro  
245 250 255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu  
260 265 270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg  
275 280 285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu  
290 295 300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro  
305 310 315 320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro  
325 330 335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu  
340 345 350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser  
355 360 365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln  
370 375 380

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val  
385 390 395 400

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu  
405 410 415

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala  
420 425 430

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu  
435 440 445

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys  
450 455 460

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys  
465 470 475 480

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe  
485 490 495

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys  
500 505 510

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys  
515 520 525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp  
530 535 540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu



Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg  
705 710 715 720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe  
725 730 735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly  
740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg  
755 760 765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu  
770 775 780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu  
785 790 795 800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val  
805 810 815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala  
820 825 830

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu  
835 840 845

Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala  
850 855 860

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr  
865 870 875 880

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln  
885 890 895

Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln  
900 905 910

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser  
915 920 925

Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser  
930 935 940

Glu Leu Gln Arg Leu Arg Arg  
945 950

<210> 173  
<211> 2796  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (574)..(1683)

<400> 173

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ttgggccttt tcttgtgtcc tgtttgttaa aggcatgcgg gctccagcat taaagagggc 120

tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg 180

tttgacgtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240

cctgtttttt gttttttgtt ttgttttgtt ttgtttttt atggataaaa atatgcgctt 300

ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360

ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc 420

ctccagaaaa ttcatlgatt atccaagtct cagataaatc tggtgccaga gtttggtttg 480

aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaaccctt 540

gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594

Met Gly Asp Arg Arg Phe Ile

1

5

gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642

Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly

10

15

20

aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690

Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr  
25 30 35

aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738  
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile  
40 45 50 55

acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786  
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg  
60 65 70

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt 834  
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu  
75 80 85

ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac 882  
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His  
90 95 100

tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc 930  
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu  
105 110 115

acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat 978  
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp  
120 125 130 135

cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc 1026  
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr

140

145

150

agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc 1074

Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu

155

160

165

agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat 1122

Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn

170

175

180

gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca 1170

Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr

185

190

195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att 1218

Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile

200

205

210

215

cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc 1266

Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu

220

225

230

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg 1314

Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val

235

240

245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta 1362

Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val

250

255

260



cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc 1410

Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala

265

270

275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att 1458

Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile

280

285

290

295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat 1506

Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr

300

305

310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554

Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His

315

320

325

ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa 1602

Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys

330

335

340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650

Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn

345

350

355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703

Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe

360

365

370

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

ttgaagctaa tgatactgag aatagagtaa tgtaccaaata gcagtcagat acatttggtt 1823

gaacactatt gtacatattc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

acaaaaacag atcagcctct tctgttgagt tgacttttca ttacctaat gaccagtggc 1943

cttgactttt agtgatgtga gggttatttt taaacttaaa aaaaaaggca ttccagtaat 2003

tttggttaatt gggttgggcc tataaatata gaacaattc agggattatt taaaaacatc 2063

tgtgttacta ctgatatatg ctagtatttt tttccttttt tgaattaata ttgaatttat 2123

tttaaaaaaa gaactatttt tacctaattc taataagaca tactgagaaa gagaaatgtg 2183

ttgaatttta aaatattggc aaattttacc tagattttta aaacctaat gaagtgtttg 2243

aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303

attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttaaaa aaaaaaaaaac tttaagcaac actatattat ttcttaagat 2483

tttcatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatgtt 2543

aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603

attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663

ttttaaggt ggtggtaga tagctgtaat ttgaaatcc atactctctt ctgtacattt 2723

tggagcacat ttagccaag gcgctgctga atttgtgctc aggtcgggag catattgaaa 2783

aagatgtgta cat 2796

<210> 174

<211> 370

<212> PRT

<213> Homo sapiens

<400> 174

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe

50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn

65

70

75

80

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile

85

90

95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys

100

105

110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe

115

120

125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe

130

135

140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala

145

150

155

160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe

165

170

175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe

180

185

190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile

195

200

205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser

210

215

220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile  
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala  
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr  
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe  
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys  
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys  
305 310 315 320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr  
325 330 335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu  
340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser  
355 360 365

Thr Phe  
370

<210> 175  
 <211> 2299  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (67)..(1176)

<400> 175

cctaccggtc catagtgtca gagtgggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser

1 5 10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156

Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr

15 20 25 30

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204

Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr

35 40 45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252

Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe

50

55

60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300

Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile

65

70

75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348

Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe

80

85

90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396

Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu

95

100

105

110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444

Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met

115

120

125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492

Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr

130

135

140

cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg 540

Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val

145

150

155

tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct 588

Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser

160

165

170

ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa 636

Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu

175 180 185 190

ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata 684

Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile

195 200 205

ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct 732

Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser

210 215 220

tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct 780

Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser

225 230 235

caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat 828

Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His

240 245 250

atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc 876

Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe

255 260 265 270

ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa 924

Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu

275 280 285



aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg 972

Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu

290

295

300

aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt 1020

Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe

305

310

315

cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt 1068

Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe

320

325

330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa 1116

Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln

335

340

345

350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta 1164

Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu

355

360

365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc 1216

Glu Ser Thr Phe

370

ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaatacca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt 1336

gttcagtaat tataggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttg aatttcattg tatcgatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tattttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgta 1696

tgtgcatttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcggt 1816

gtttttacac caaattaataa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gccaggtca ggagcaaatt gaaaaaaaa ataaagtaat actaaaaaat 2116

caaactataa acccaaaaca tttattaataa cctgaattaa tccttttttg aggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaatt aaaaaaaaaa aaaaaaaatt 2296

cct

2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser  
1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile  
20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val  
35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe  
50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn  
65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile  
85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys  
100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe  
115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe  
130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala  
145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe  
165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe  
180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile  
195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser  
210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile  
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala  
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr  
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe  
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys  
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys  
305 310 315 320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr  
325 330 335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu  
340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser  
355 360 365

Thr Phe  
370

<210> 177

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)..(416)

<400> 177

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Met Ala Arg Gly Ser Leu Arg Arg

1 5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101

Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser

10 15 20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149

Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser

25 30 35 40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197

Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg

45 50 55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245

Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro

60 65 70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293

Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu

75

80

85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341

Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys

90

95

100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389

Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

105

110

115

120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgccca 436

Gly Cys Pro Ala Val Ala Leu Ile Gln

125

gccggggctc gccactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcgggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc 616

tccagaacag aaaggagcc tcacgtggc tcacacaaaa cagctgacac tgactaagga 676

actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc ccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856

ggagggctgg ccctaagata cagaccccc caactcccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggagggagaa tttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly  
1 5 10 15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly  
20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys  
35 40 45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys  
50 55 60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro  
65 70 75 80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser  
85 90 95



Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile  
115 120 125

Gln

<210> 179

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 179

cttctgctct aaaagctgcg

20

<210> 180

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 180

cgacctgcag ctcgagcaca

20

【 0 1 2 9 】

【配列表フリーテキスト】

配列番号 1 7 9 : プライマー

配列番号 1 8 0 : プライマー

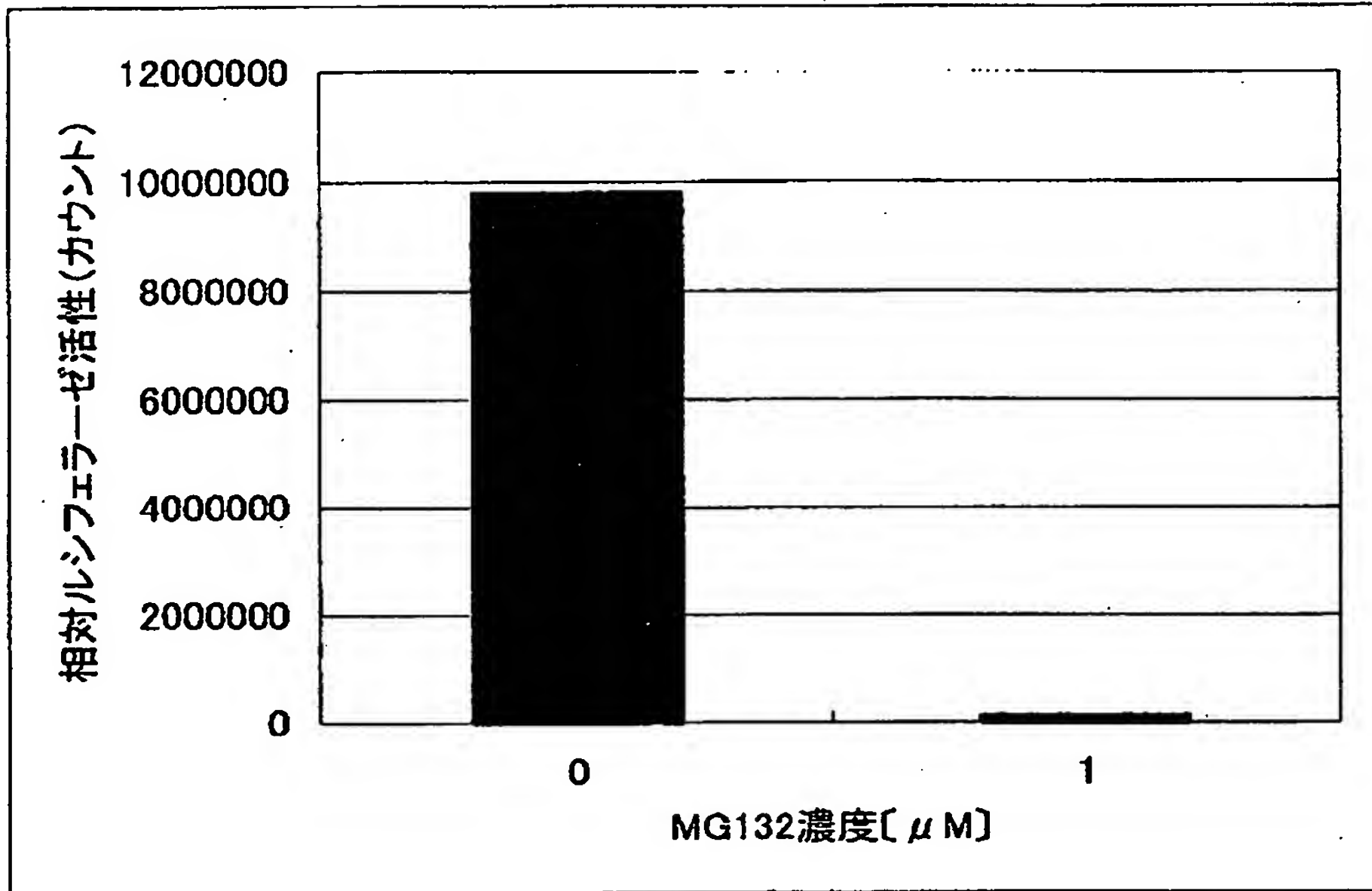
【図面の簡単な説明】

【図 1】

図 1 は、実施例 3 のプロテアソーム阻害剤 MG 1 3 2 による NF- $\kappa$ B のレポーター活性抑制を示す図である。図中で横軸は、MG 1 3 2 濃度、縦軸は、相対ルシフェラーゼ活性を示す。

【書類名】 図面

【図 1】



【書類名】 要約書

【要約】

【課題】 NF- $\kappa$ B の過剰な活性化または阻害が関与する疾患の診断、治療または予防等 to 使用される NF- $\kappa$ B 作用を有するタンパク質の提供。

【解決手段】 ヒト肺線維芽細胞から作製した cDNA ライブラリーから、プラスミド pNF $\kappa$ B-Luc を用いて、NF- $\kappa$ B を活性化する作用を有するタンパク質をコードする cDNA をクローニングして、その DNA 配列およびそれより推定されるアミノ酸配列を決定した。同タンパク質、これをコードする DNA、同 DNA を含有する組換えベクターおよび同組換えベクターを含有する形質転換体は、NF- $\kappa$ B の活性化を阻害または促進する物質のスクリーニングに使用される。

【選択図】 なし

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【手続補正 1】

【補正対象書類名】 特許願

【補正対象項目名】 発明者

【補正方法】 変更

【補正の内容】

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【プルーフの要否】   要

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